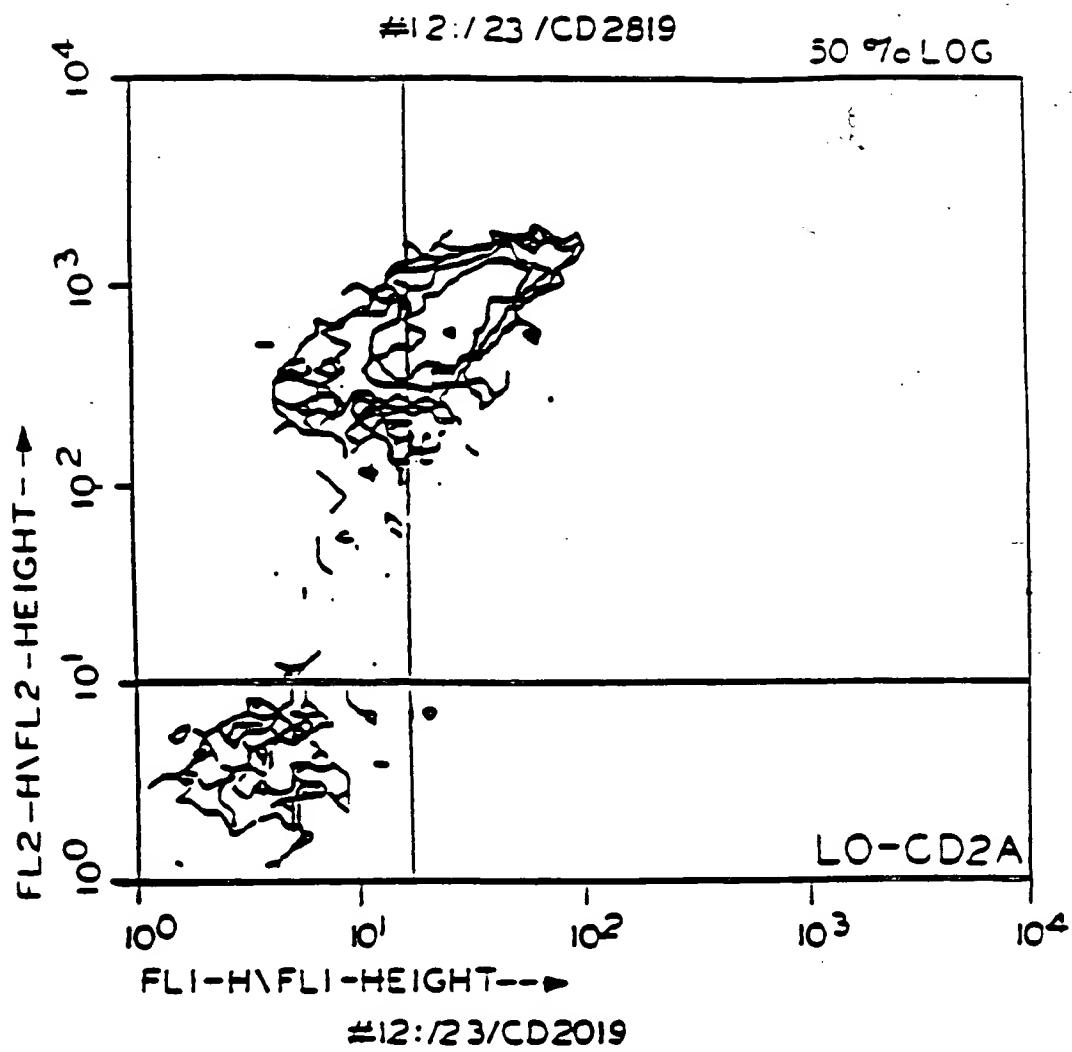


5951983



--- QUAD STATS ---

FILE: #12/23/CD2019 SAMPLE: 059

DATE: 9/24/92 GATE G1-R1

PARAMETER: FL1-H\LOG FL2-H\LOG QUAD LOCATION: 17.15.9

TOTAL = 5000 GATED = 1290

QUAD	EVENTS	% GATED	% TOTAL	X MEAN	Y MEAN
------	--------	---------	---------	--------	--------

IUL	299	23.18	3.98	11.41	284.69
2UR	831	65.97	17.02	32.70	630.65
3LL	135	10.47	2.70	4.08	3.31
4LR	5	0.39	0.10	25.11	6.54

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■ ACO CMB INST-CTRL GATES FORMAT PROTO SAVE

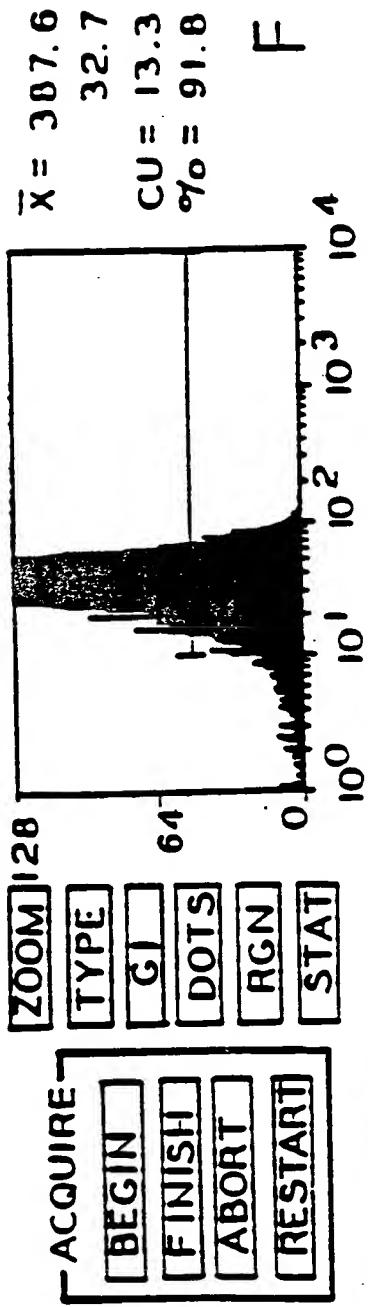
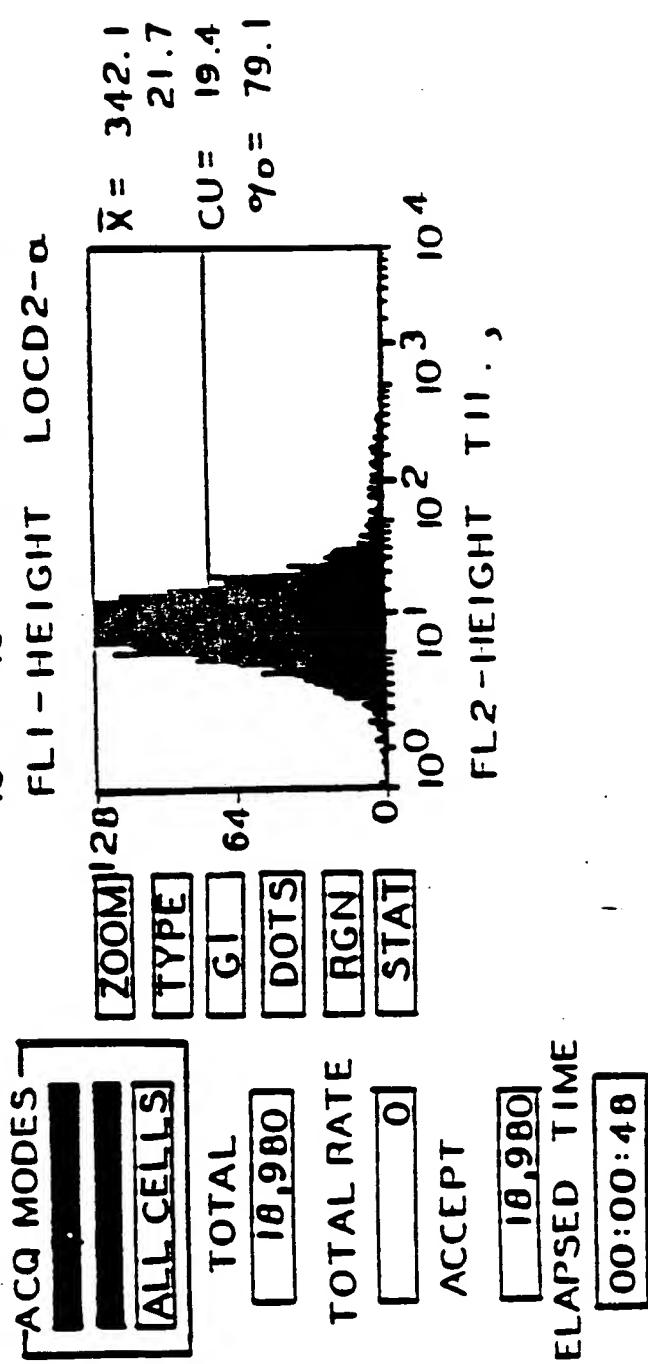


FIG. 2A



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ACO CMD INST-CTRL GATES FORMAT PROTO SAVE

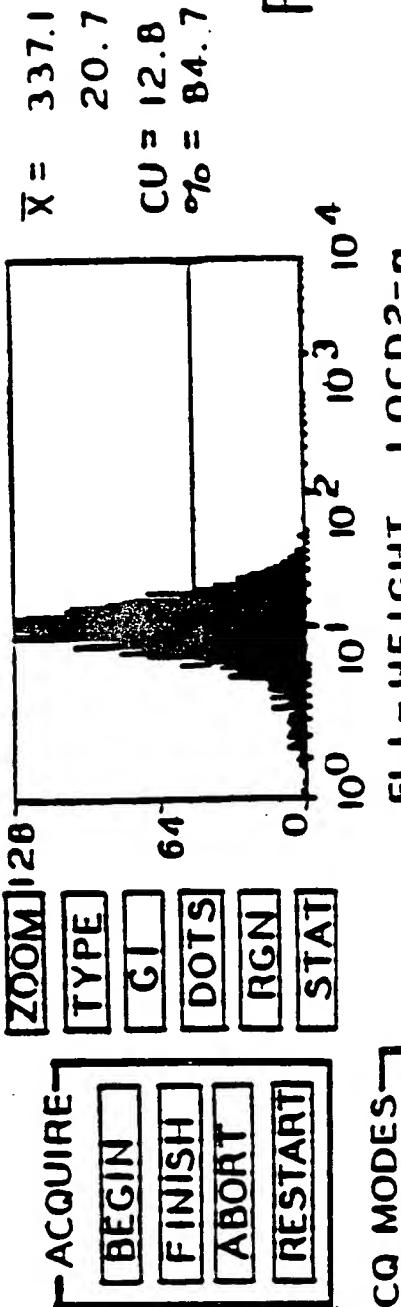
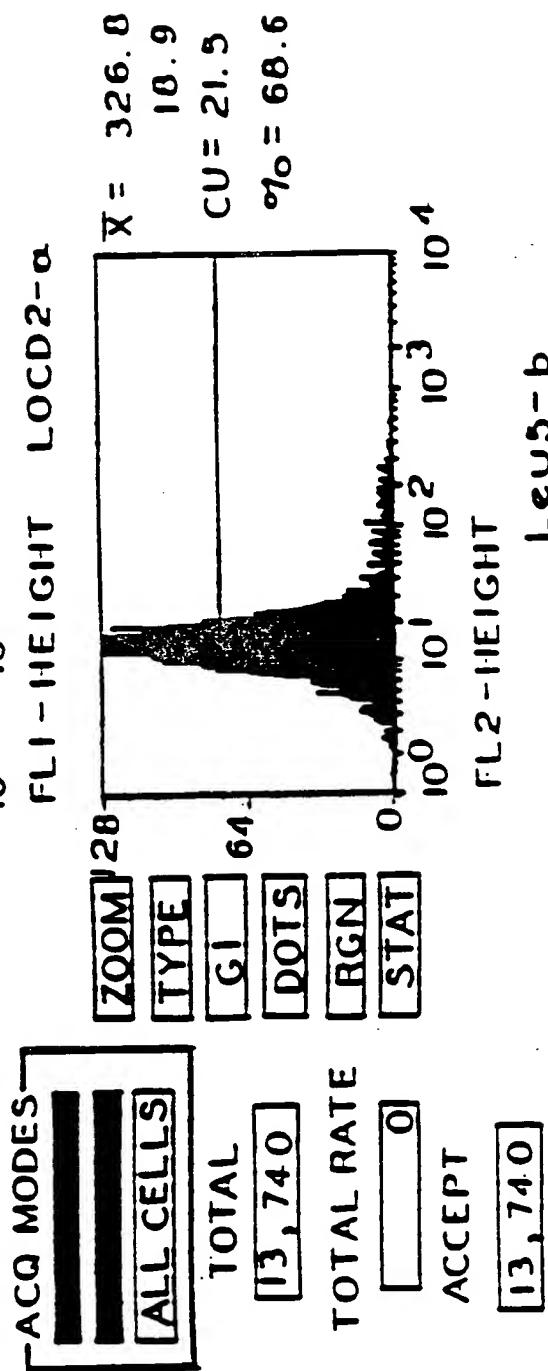
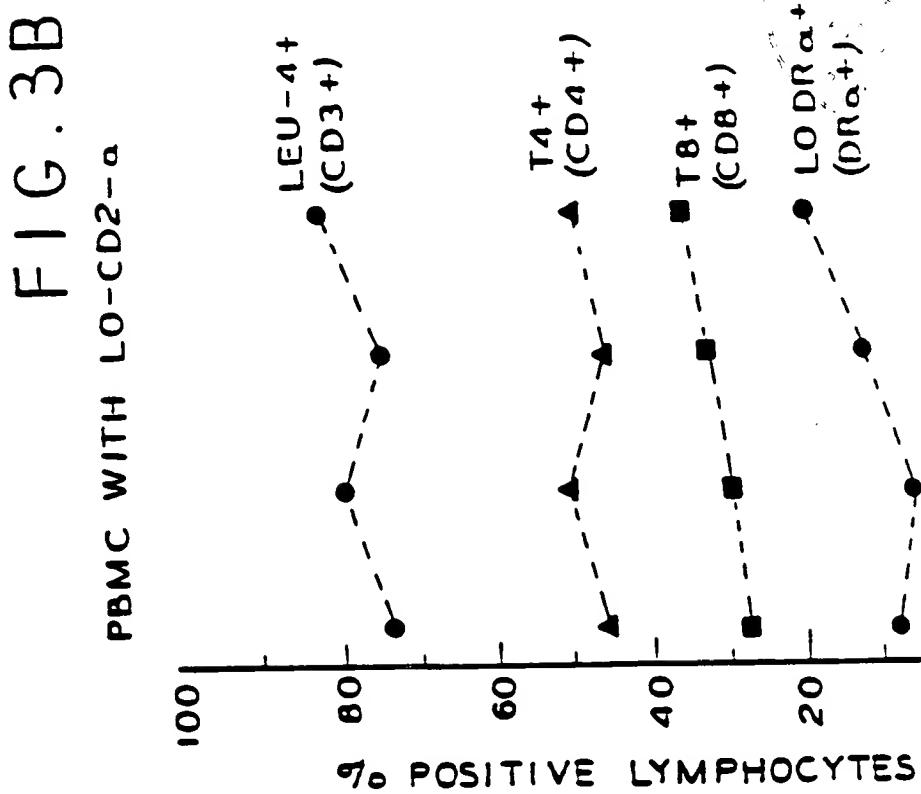
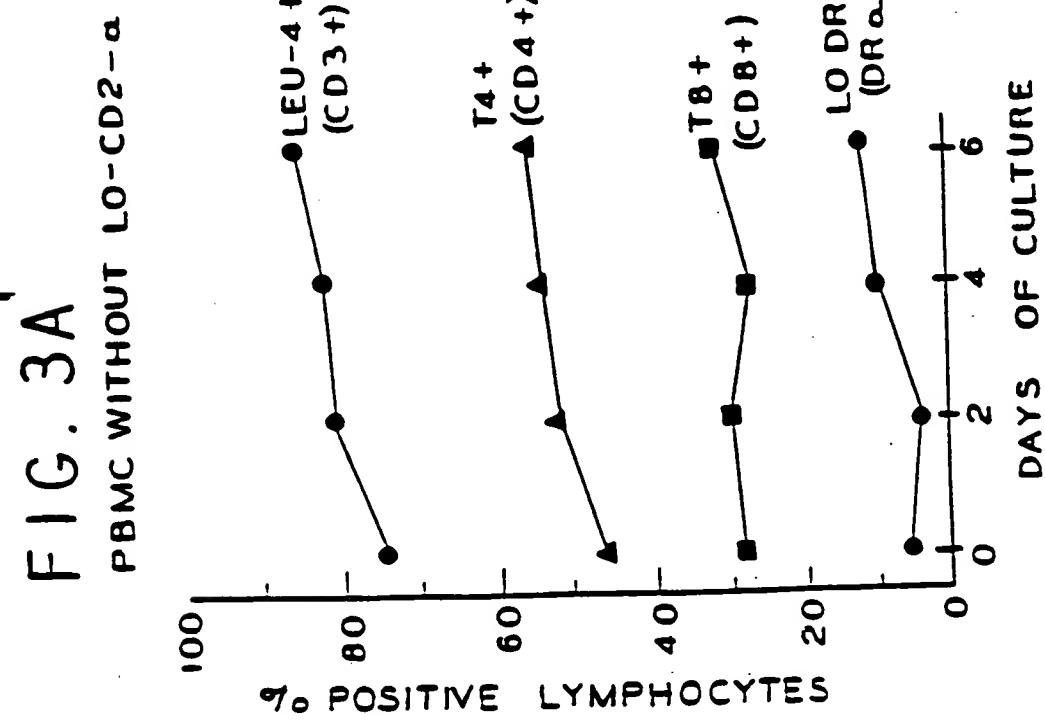


FIG. 2B



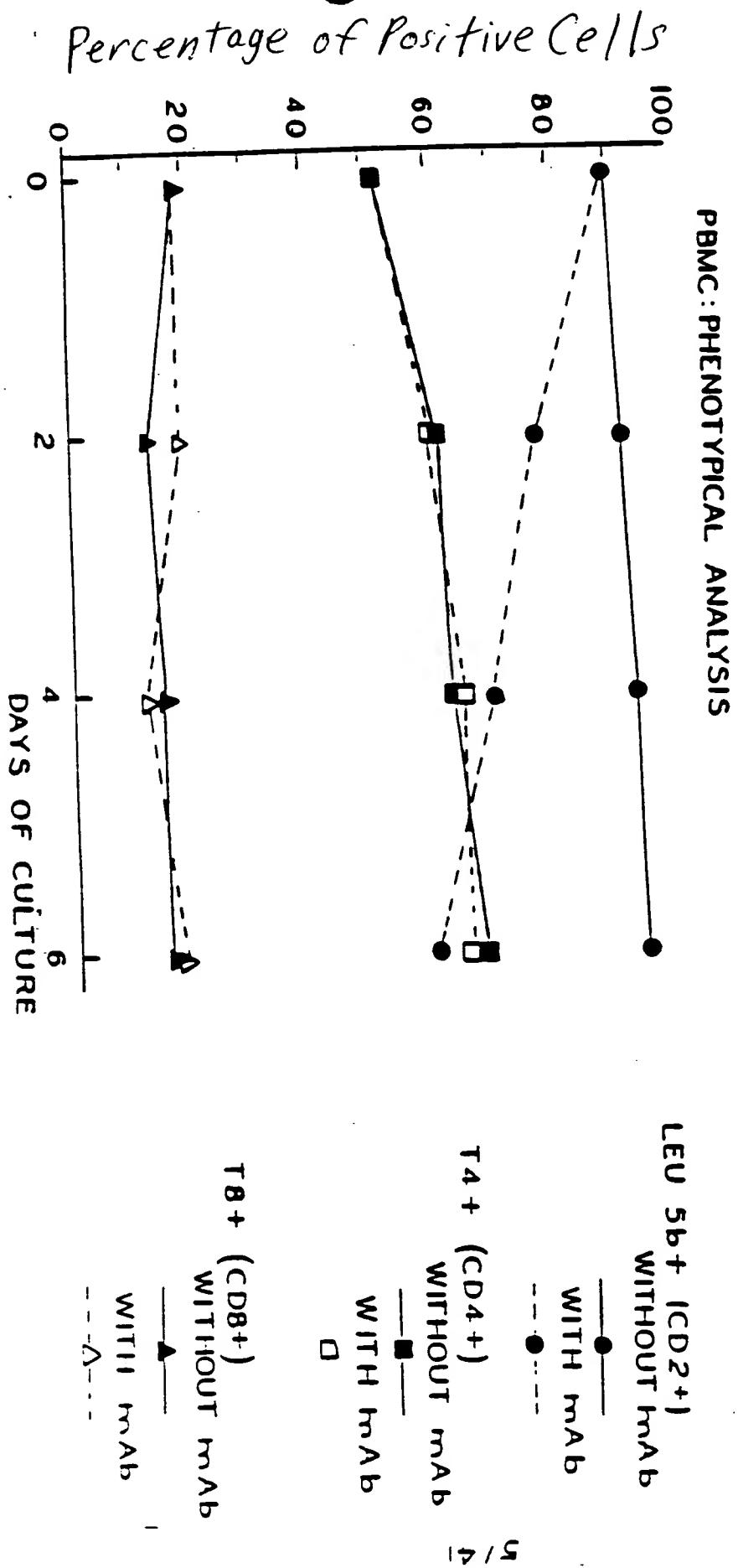
ELAPSED TIME
00:00:35



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6141

Effects of LO-CD2a on Resting
Cells during MLC

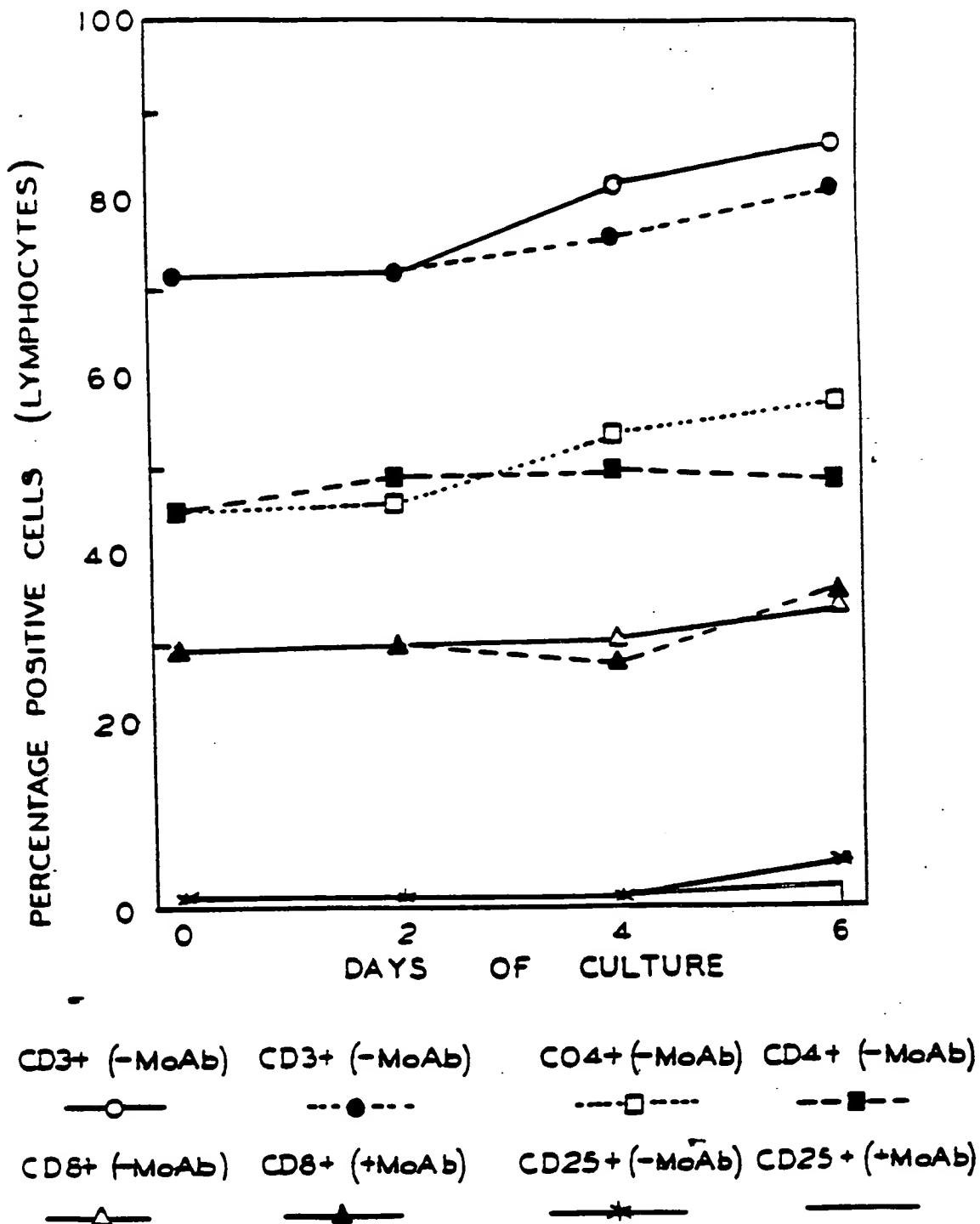


FIG. 8A

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FIG. 5B

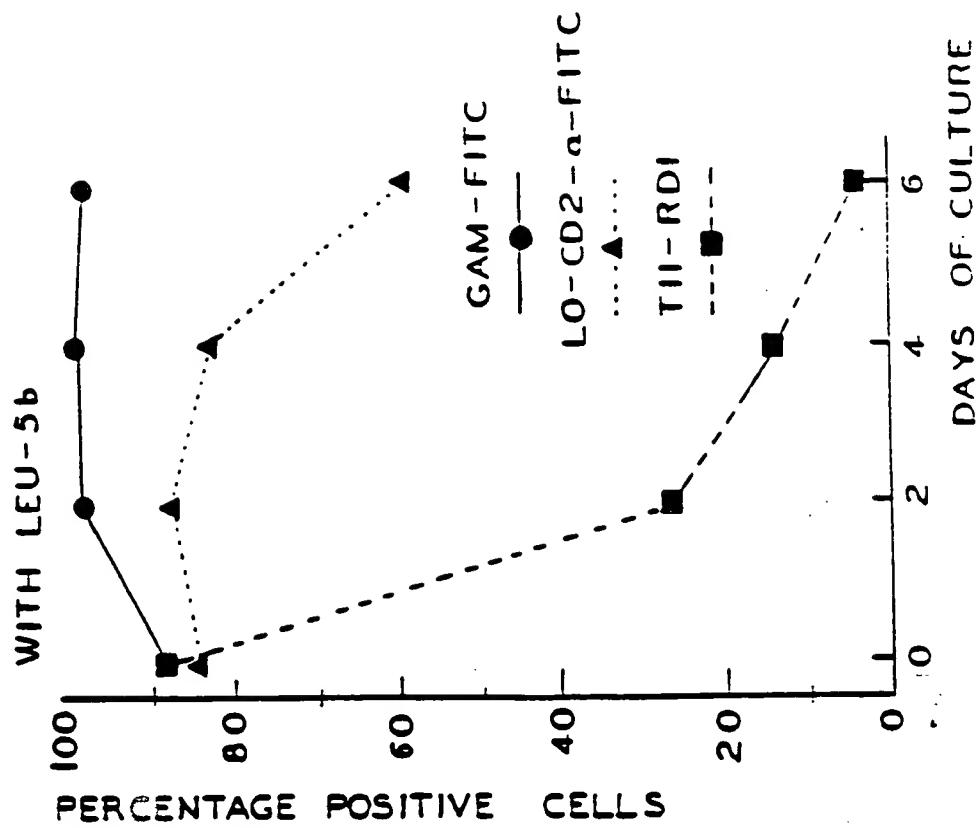
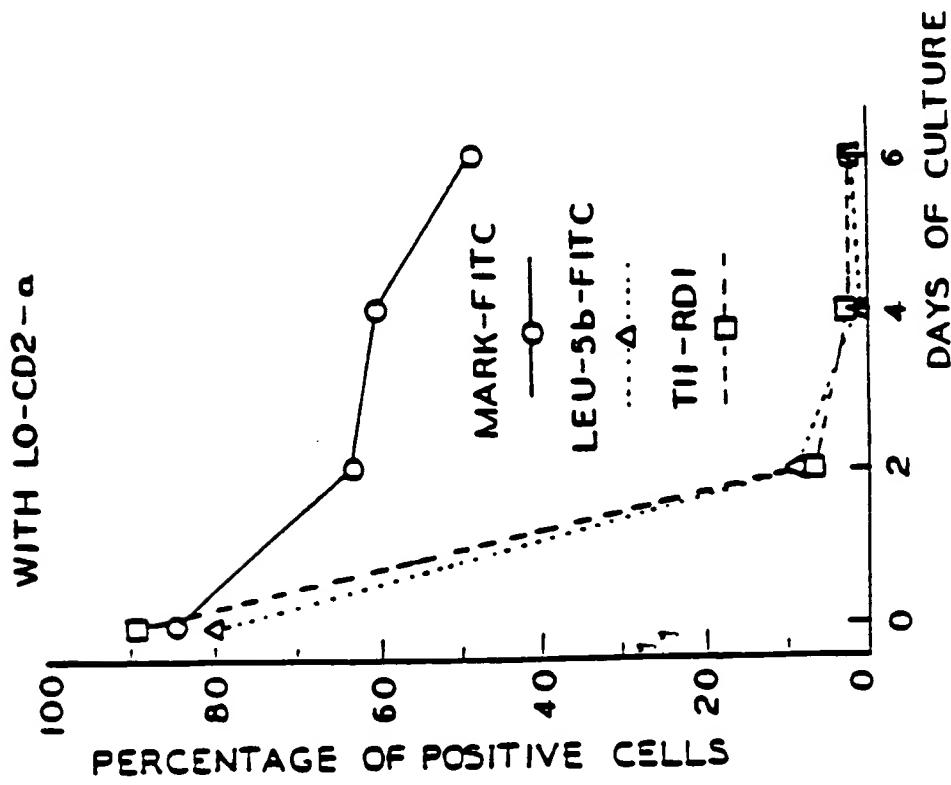


FIG. 5A



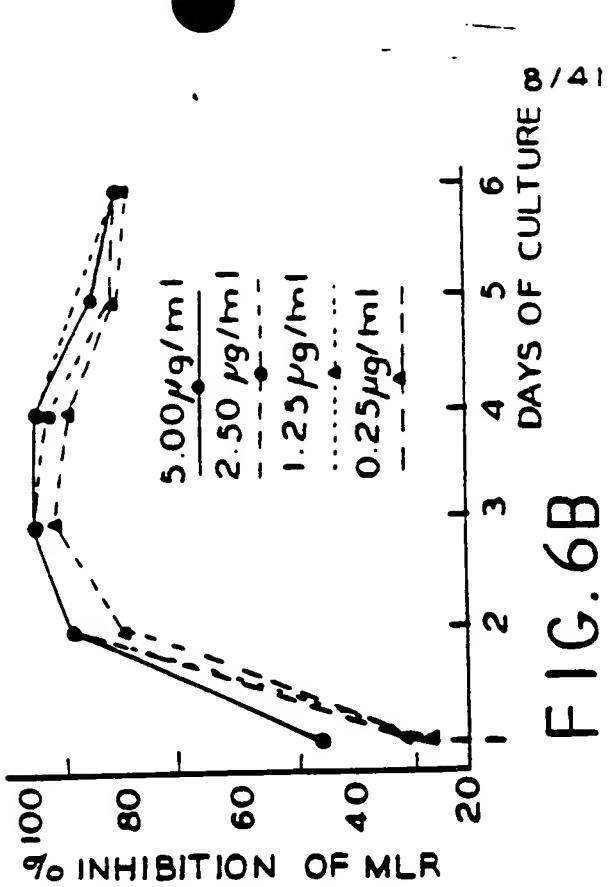


FIG. 6A

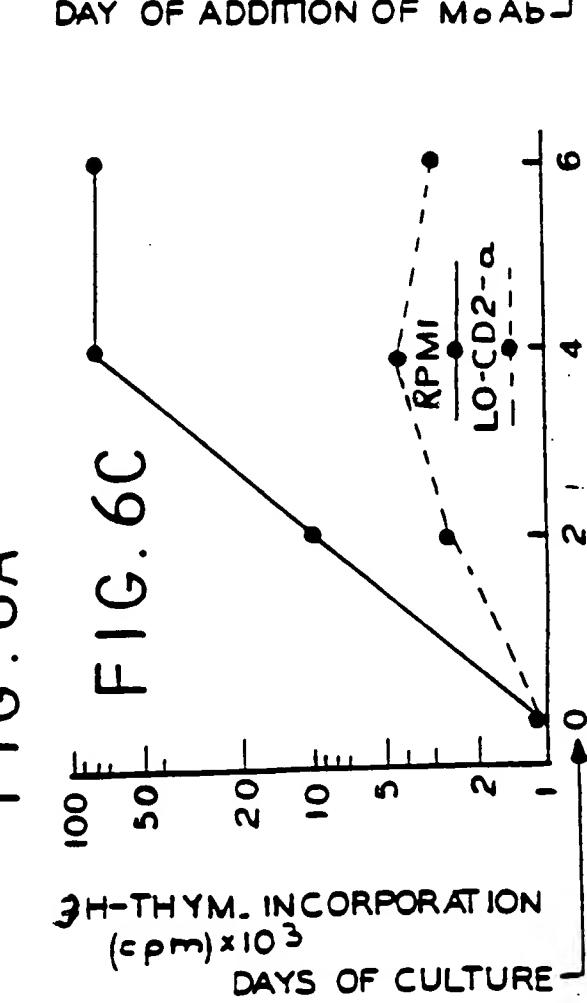


FIG. 6B

FIG. 6C

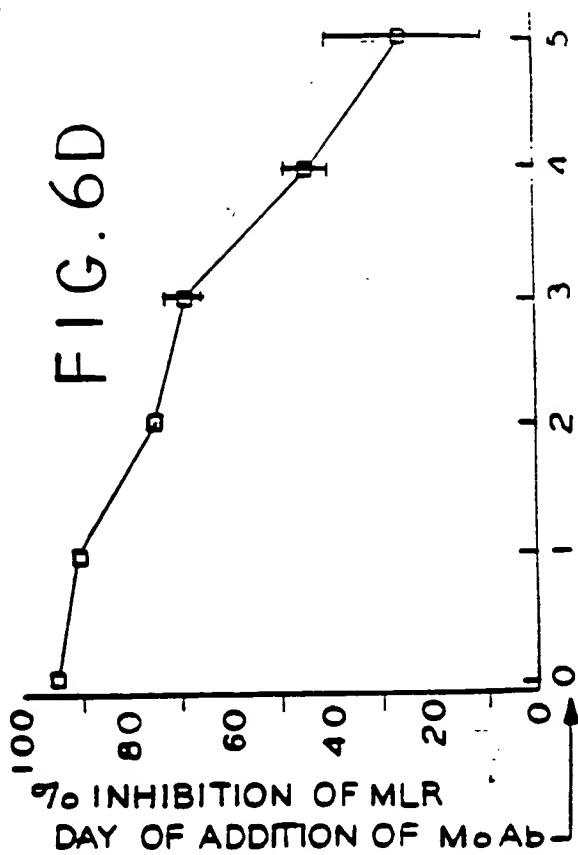


FIG. 6D

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MLC: LEU-5b+ (CD2+) CELLS

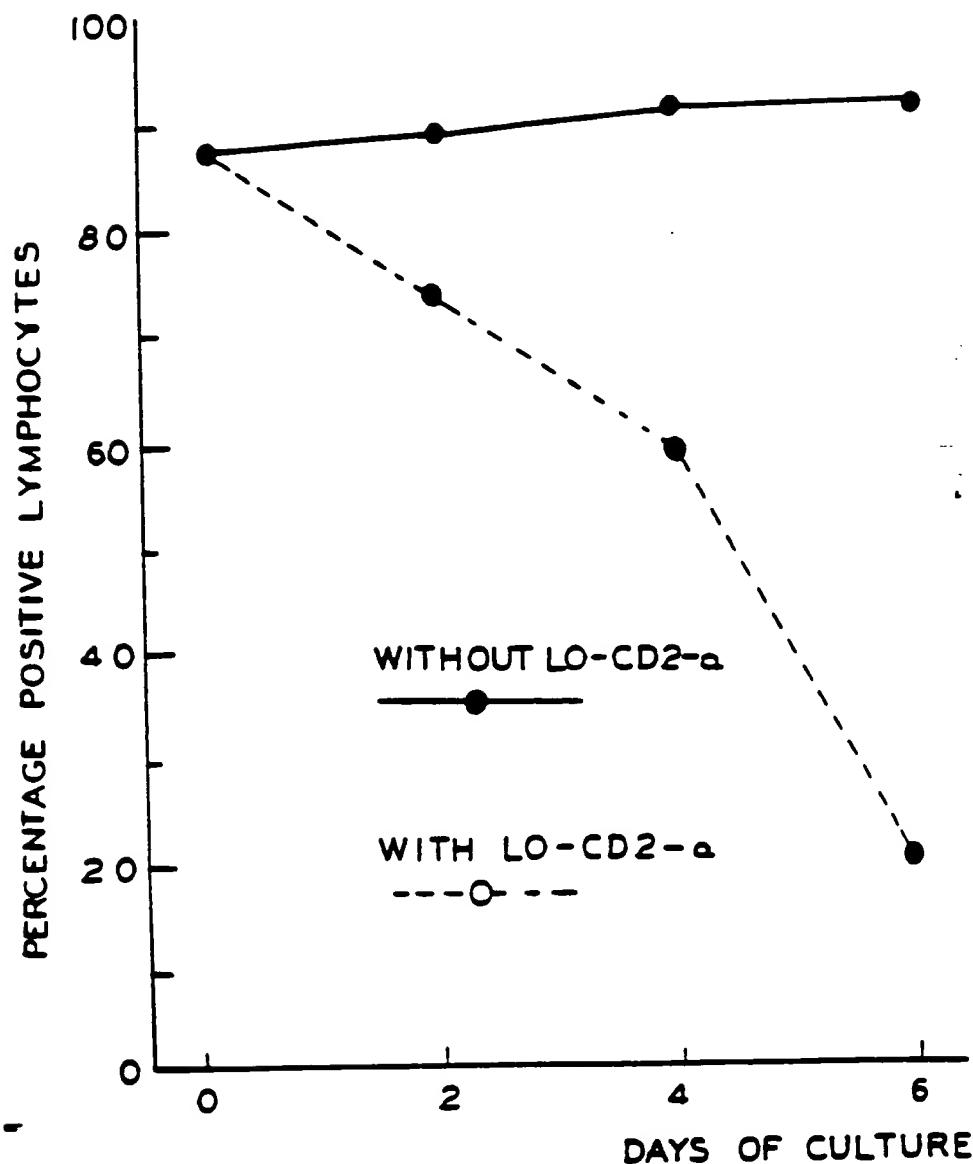


FIG. 8B

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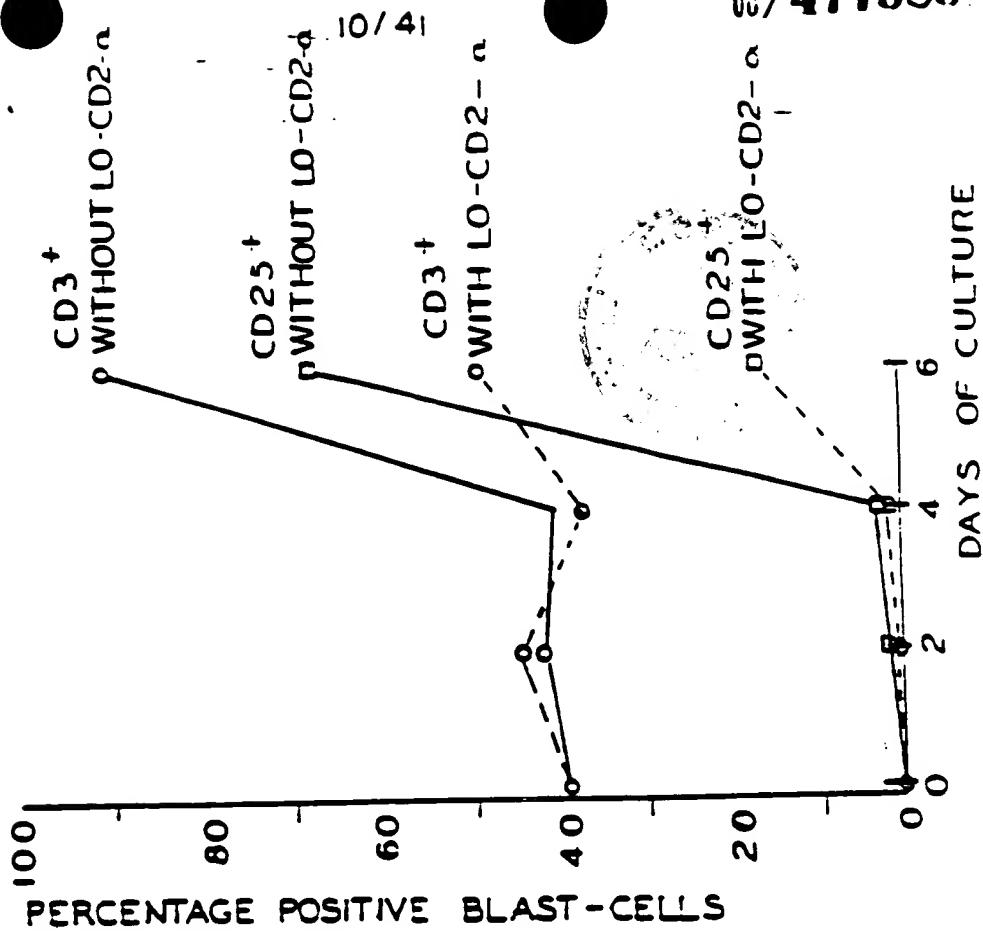
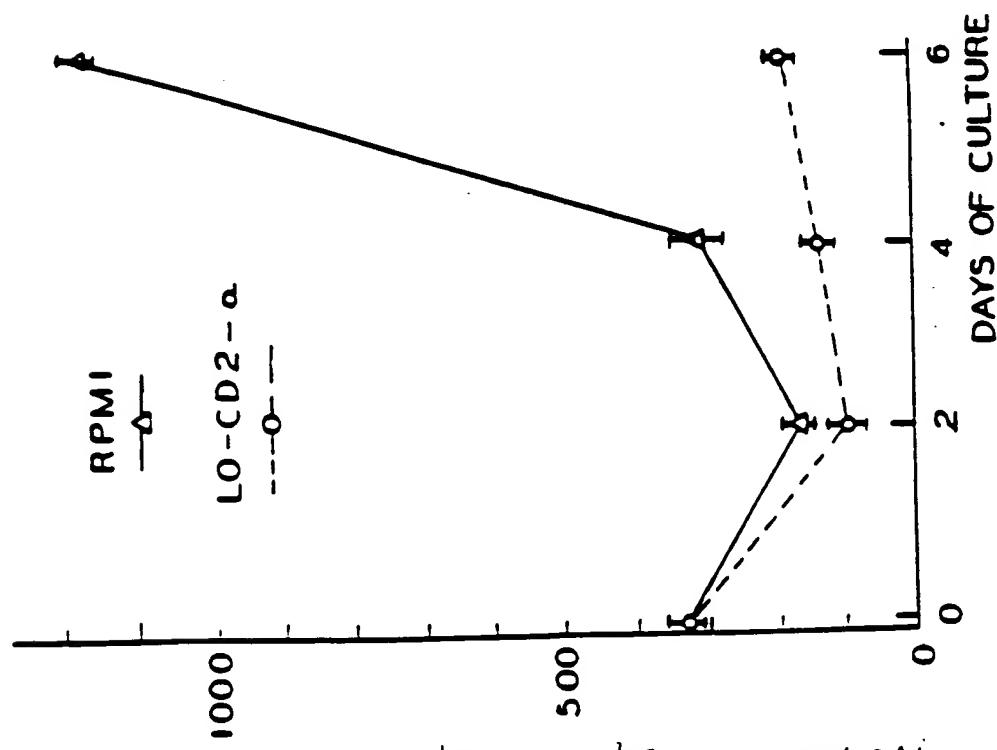


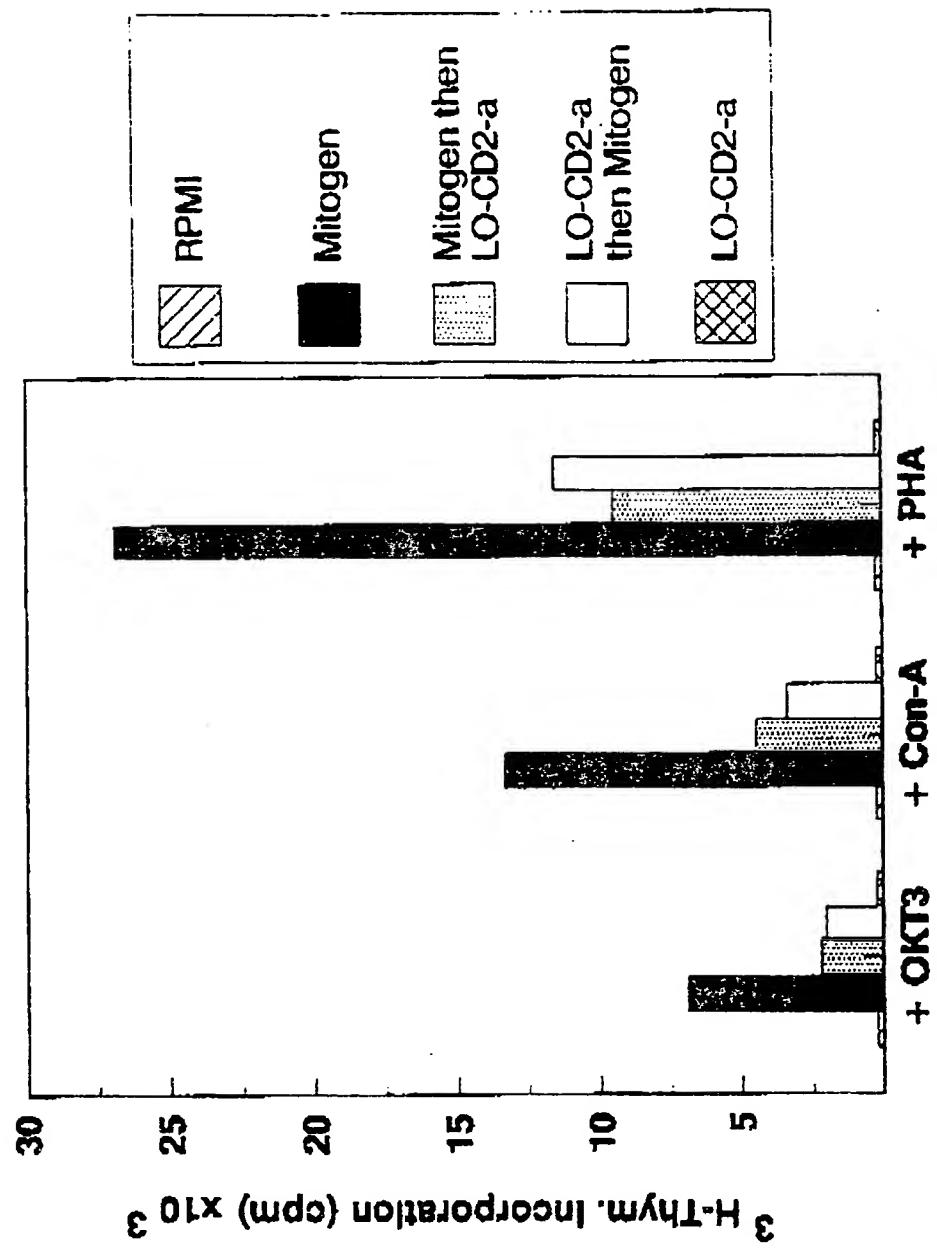
FIG. 7



Number of b/soft cell per 25,000 events analyzed

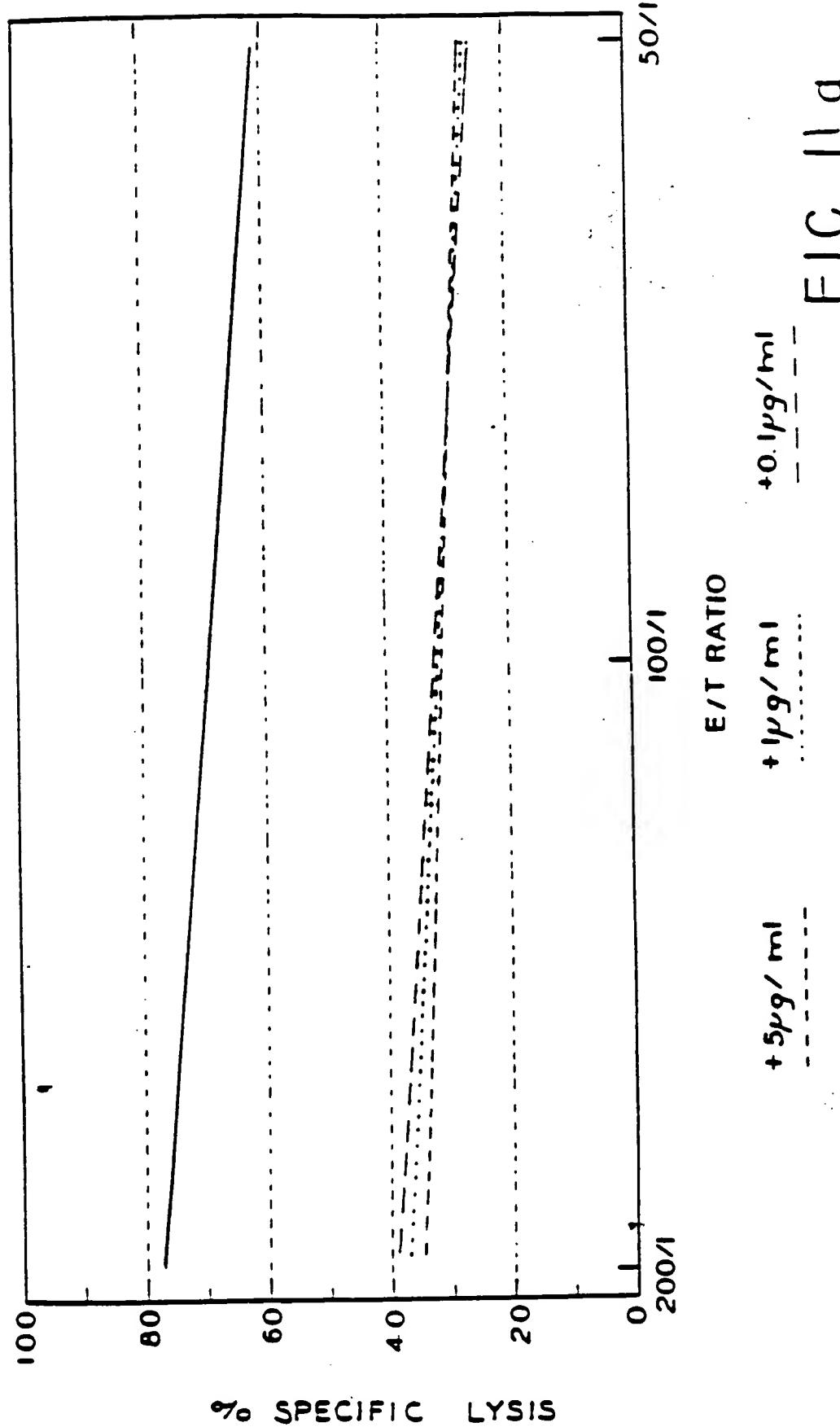
Figure 9

Effects of LO-CD2-a on mitogen-stimulated PBMC

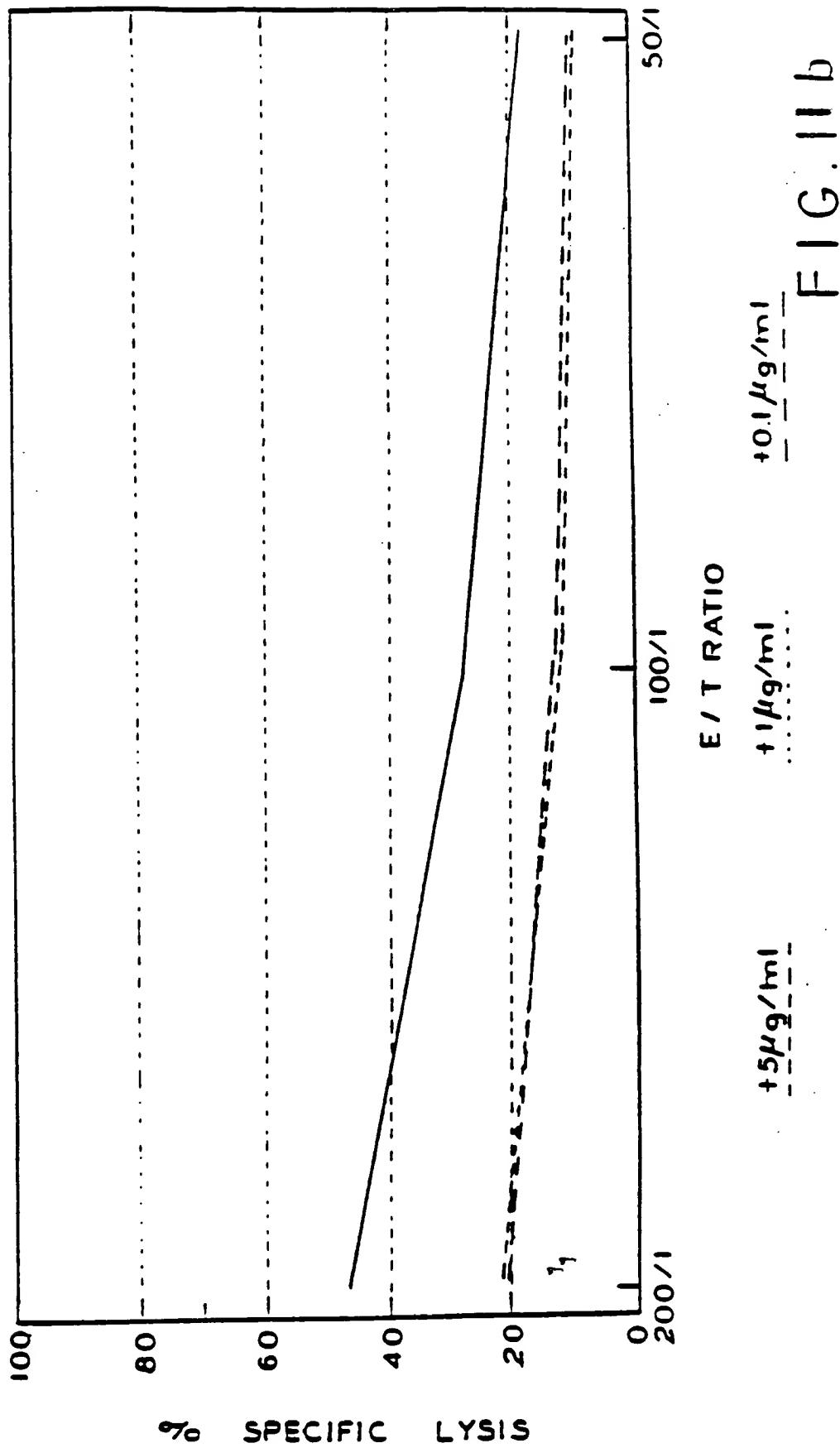


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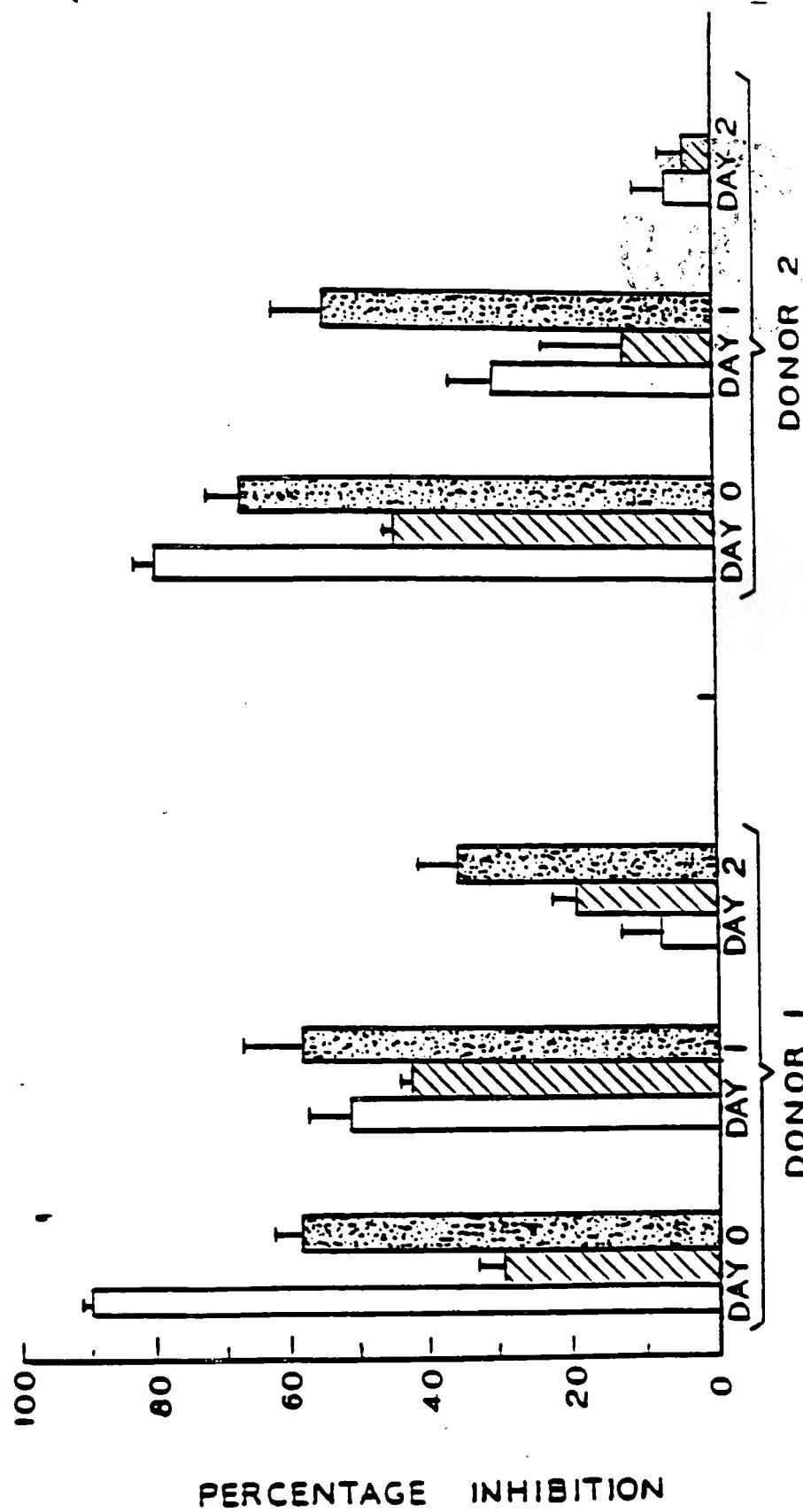


FIG. 10

OKT 3 PHA CON-A
MITOGENS ADDED AT DAY 0.

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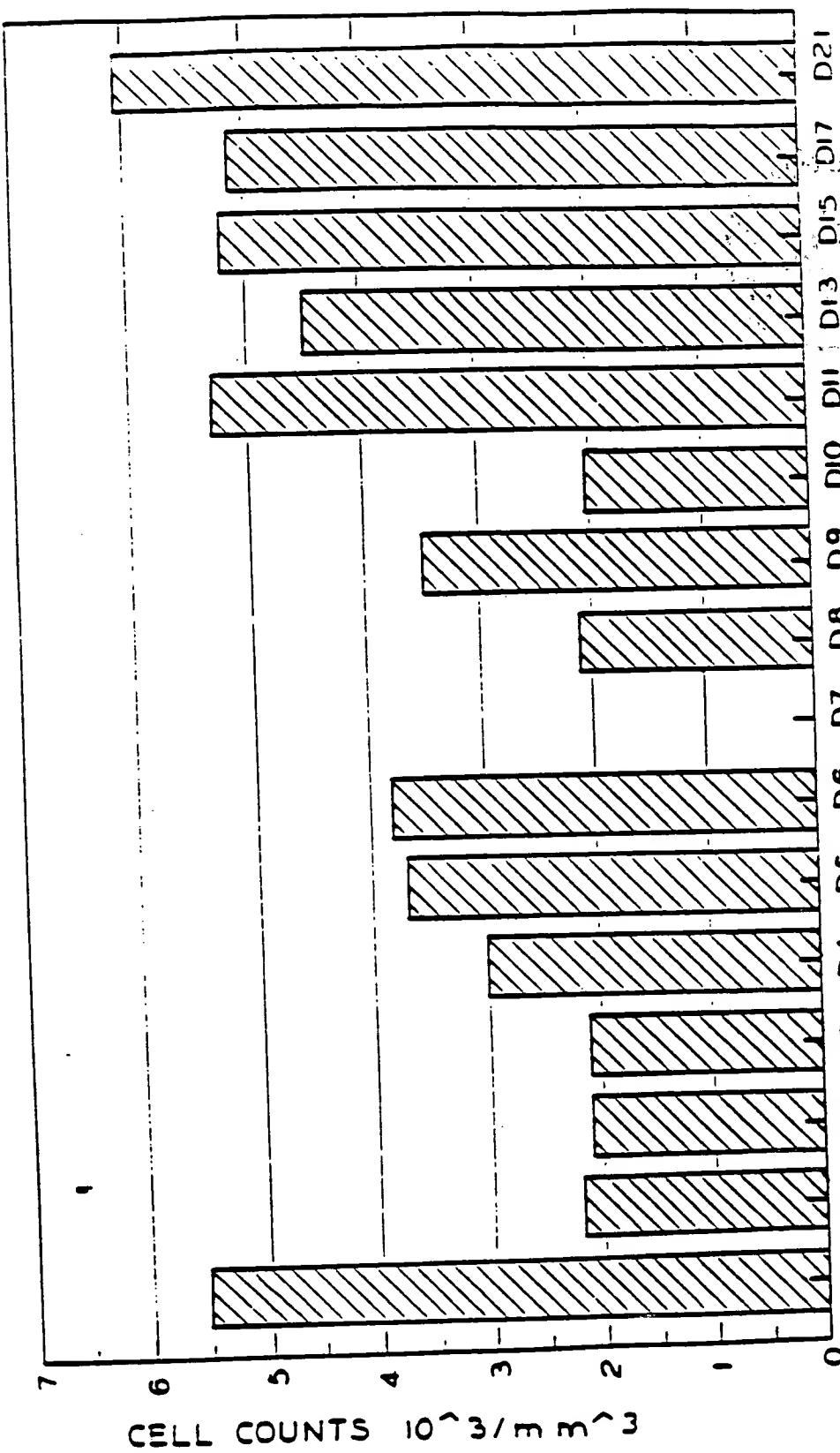
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F 1.G. 12

TIME (DAYS)

LOC D2 20mg/DAY
D0-D9

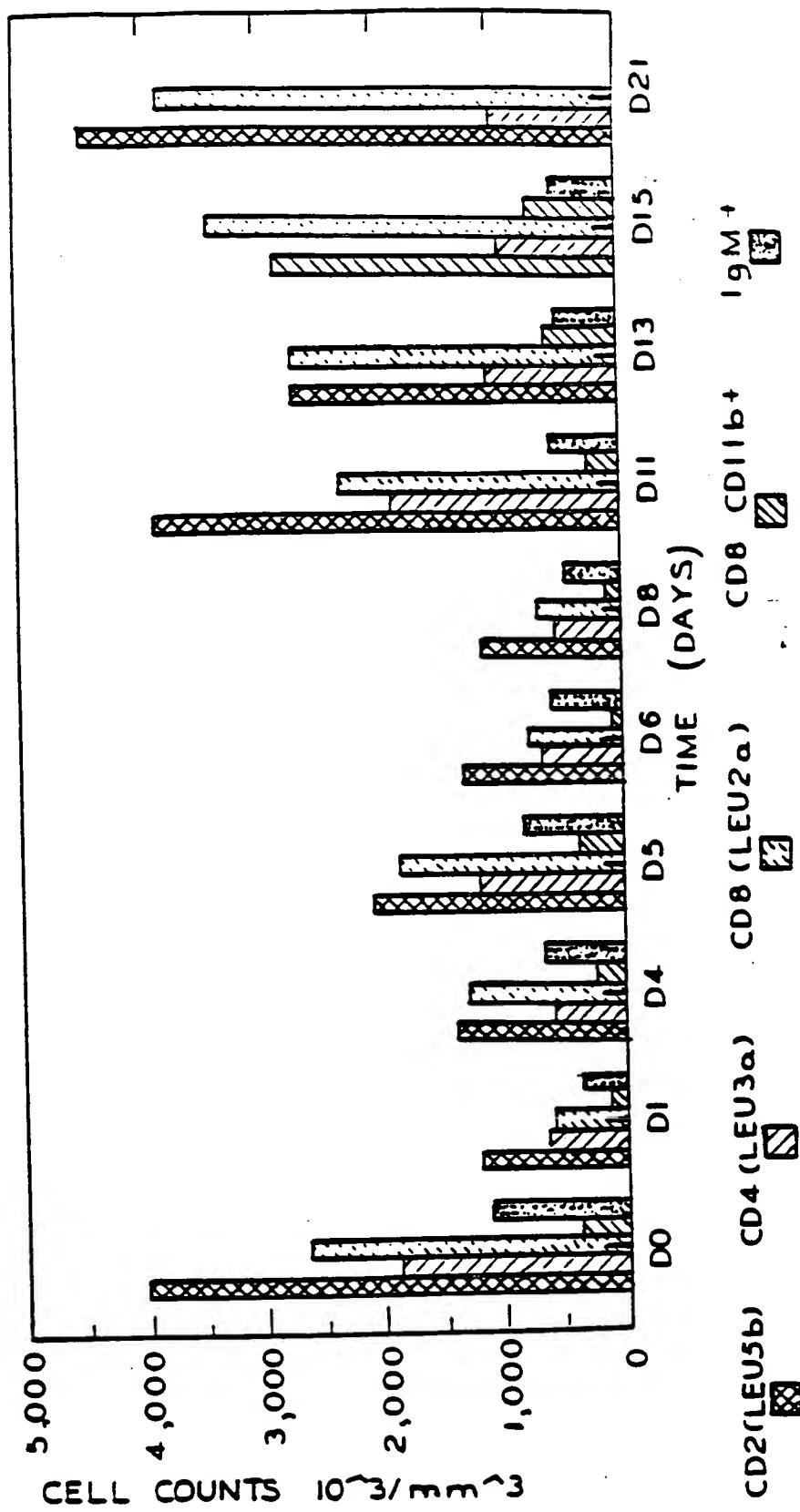
LYMPHOCYTE COUNTS



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CELL POPULATIONS FIG. 13
LOC D2: 20^{mg}/DAY
D0-D9

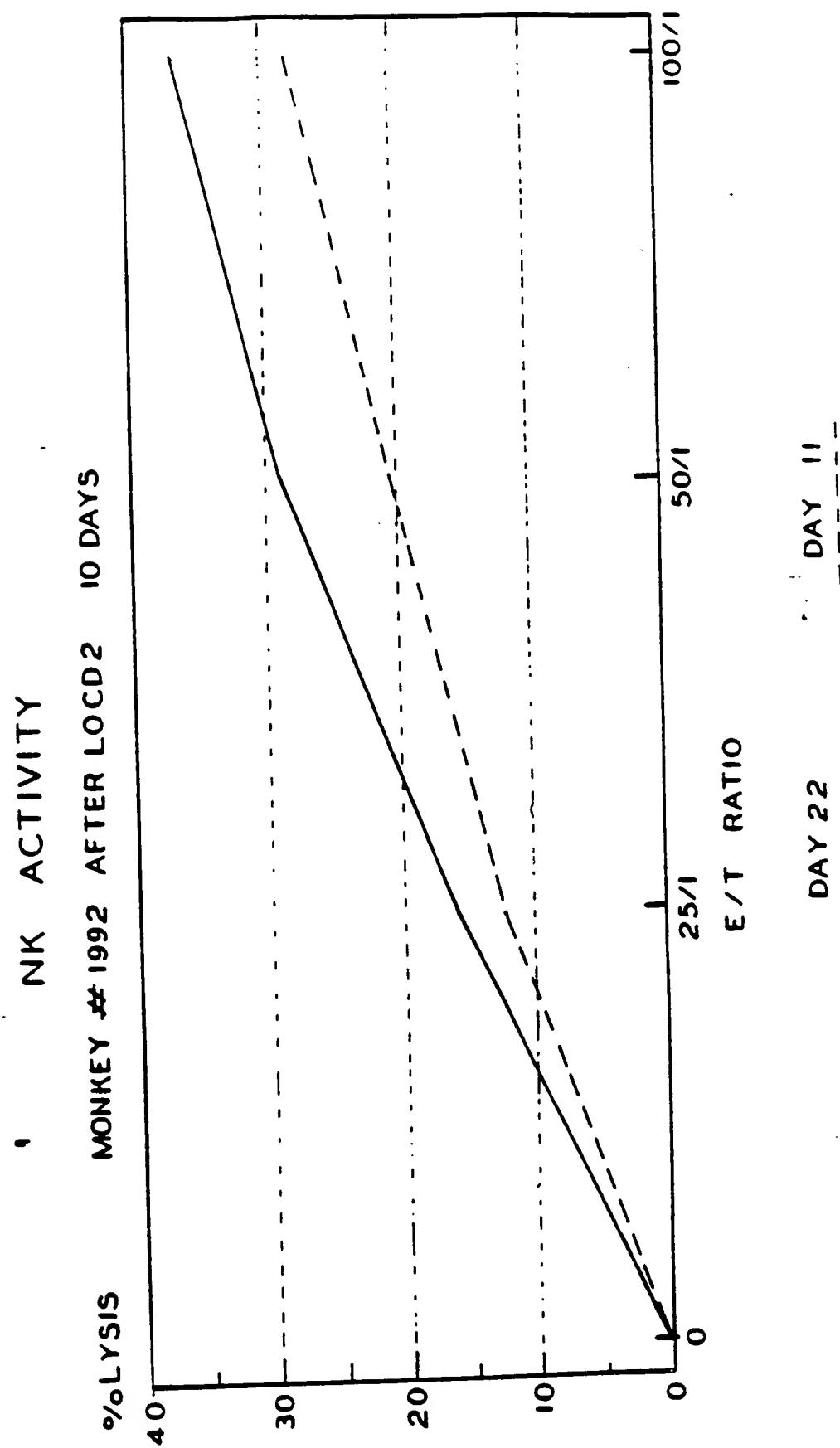


CD2 (LEU5b) : B CELLS
CD8 + CD11b + : NK CELLS
M+ : M+ CELLS

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FIG. 14



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LOCD2- α SERUM CONCENTRATION
CYNOMOLGUS MONKEY 1992

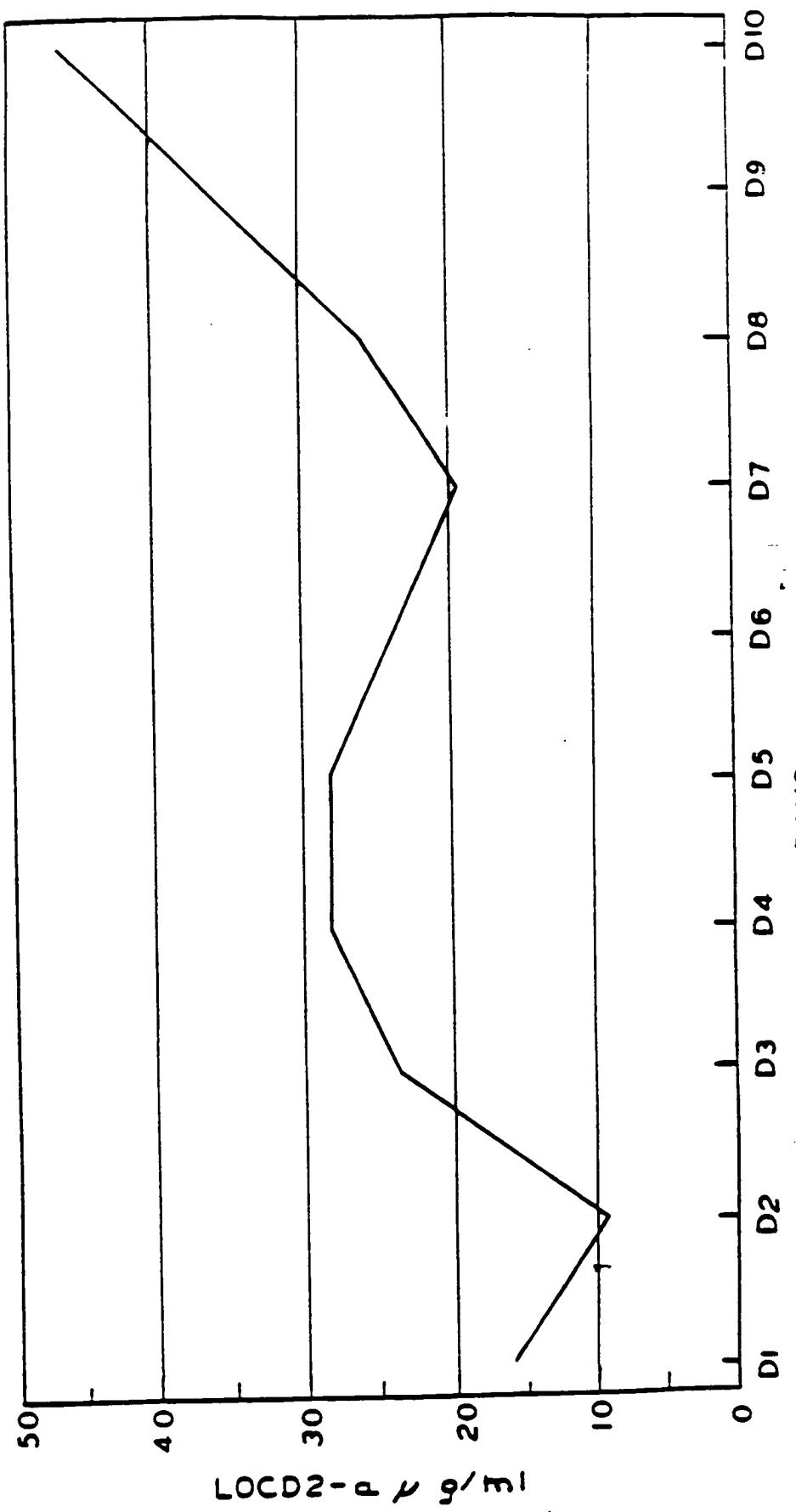
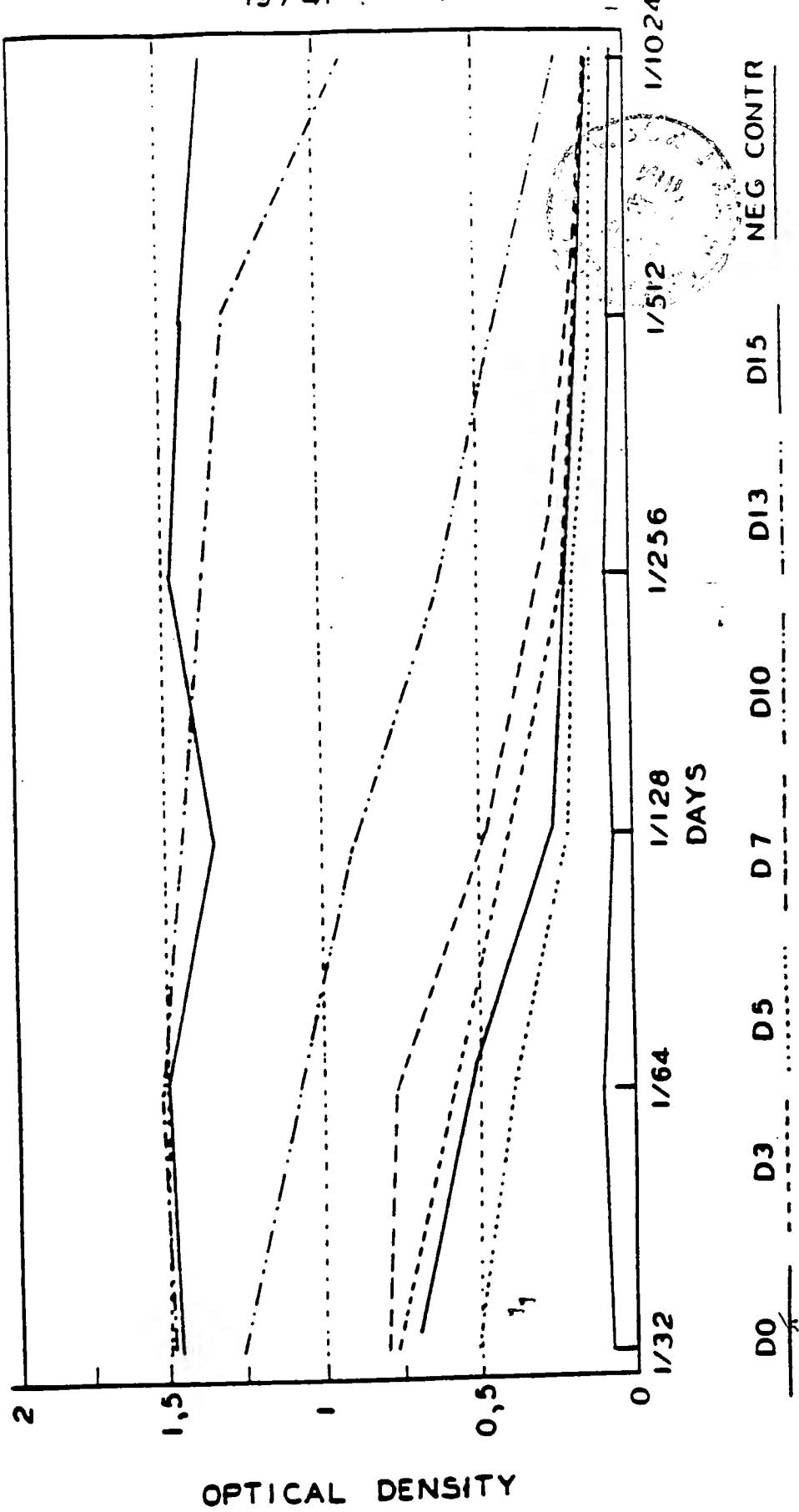


FIG. 15

FIG. 16

19G ANTIBODY ANTI-LOCD2α CYNOLOGUS MONKEY



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FIG. 17B
LO-CD2- α : SERIC DOSAGES

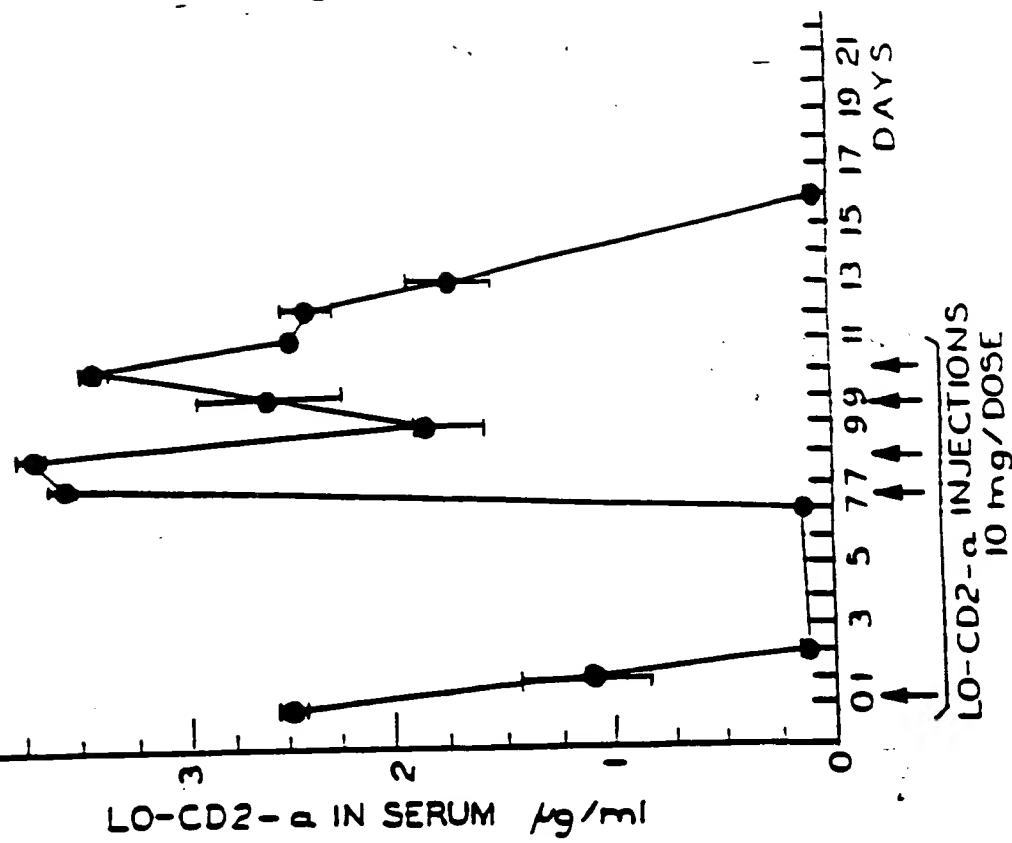


FIG. 17A
PHENOTYPICAL MARKERS

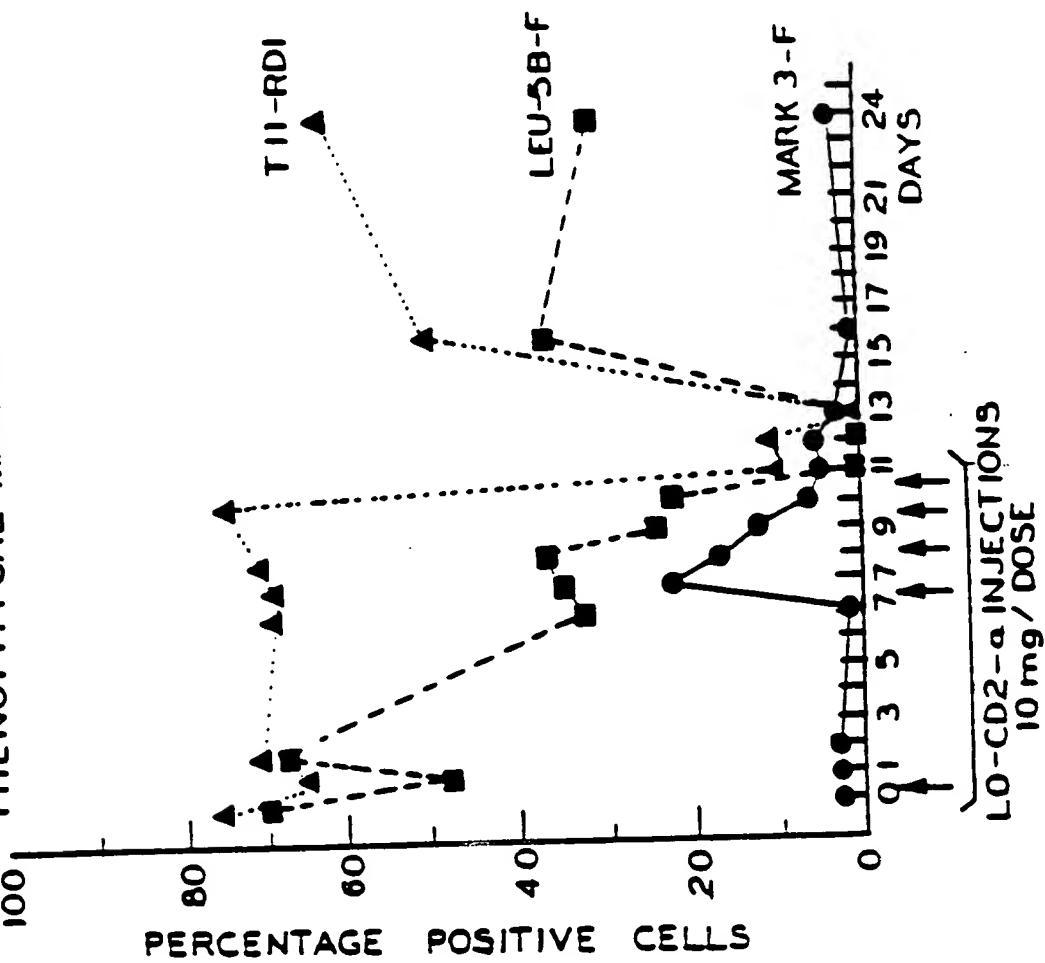


FIG. 18A

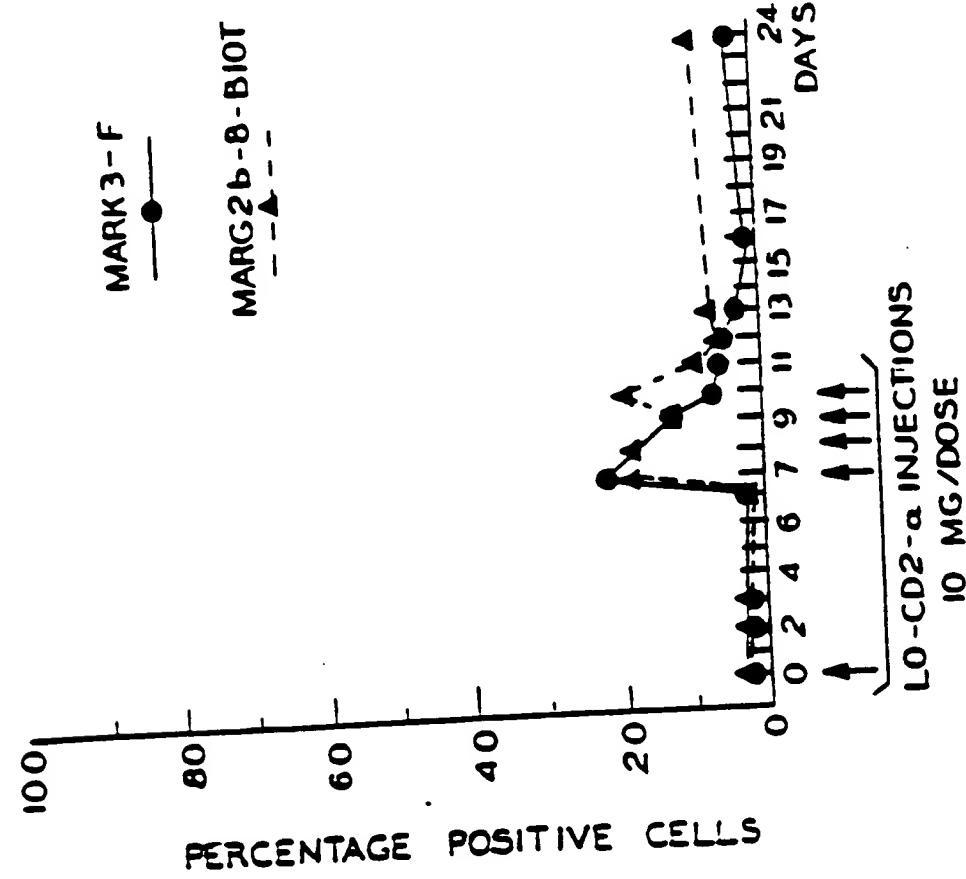
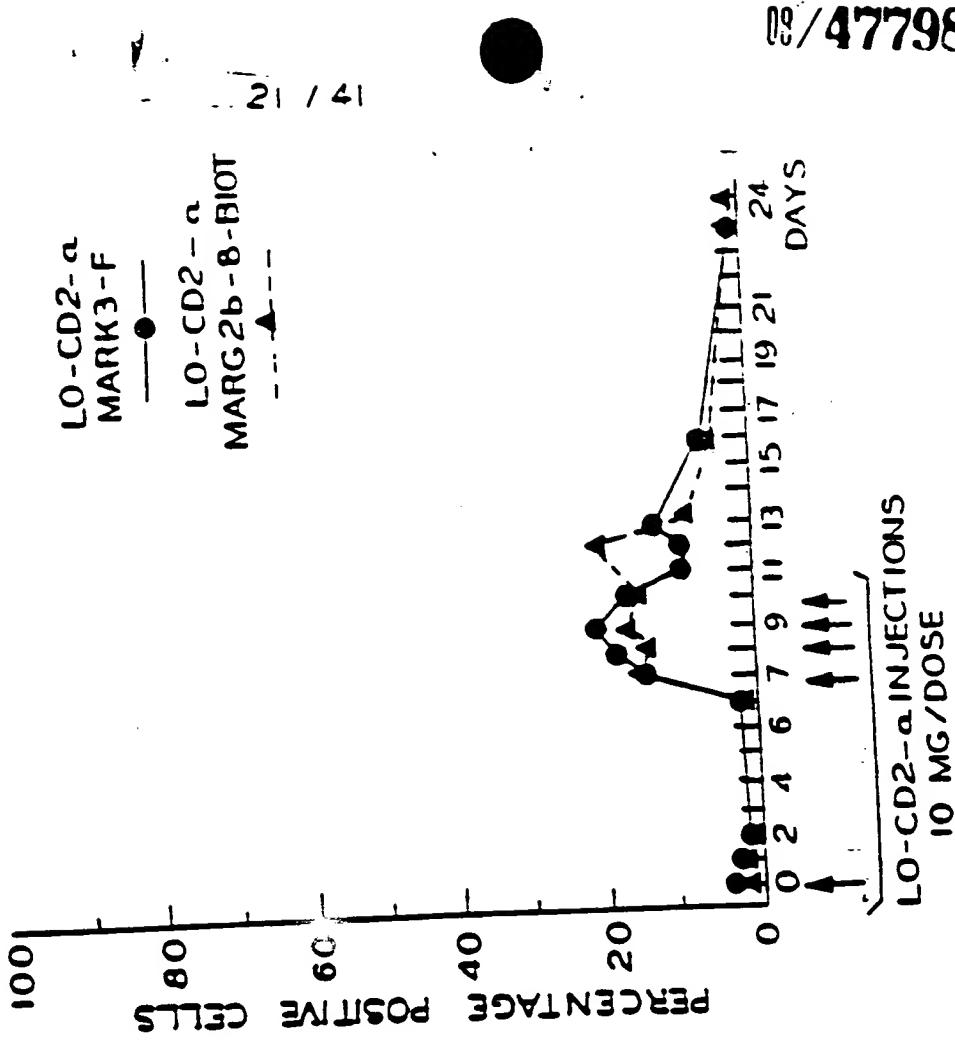


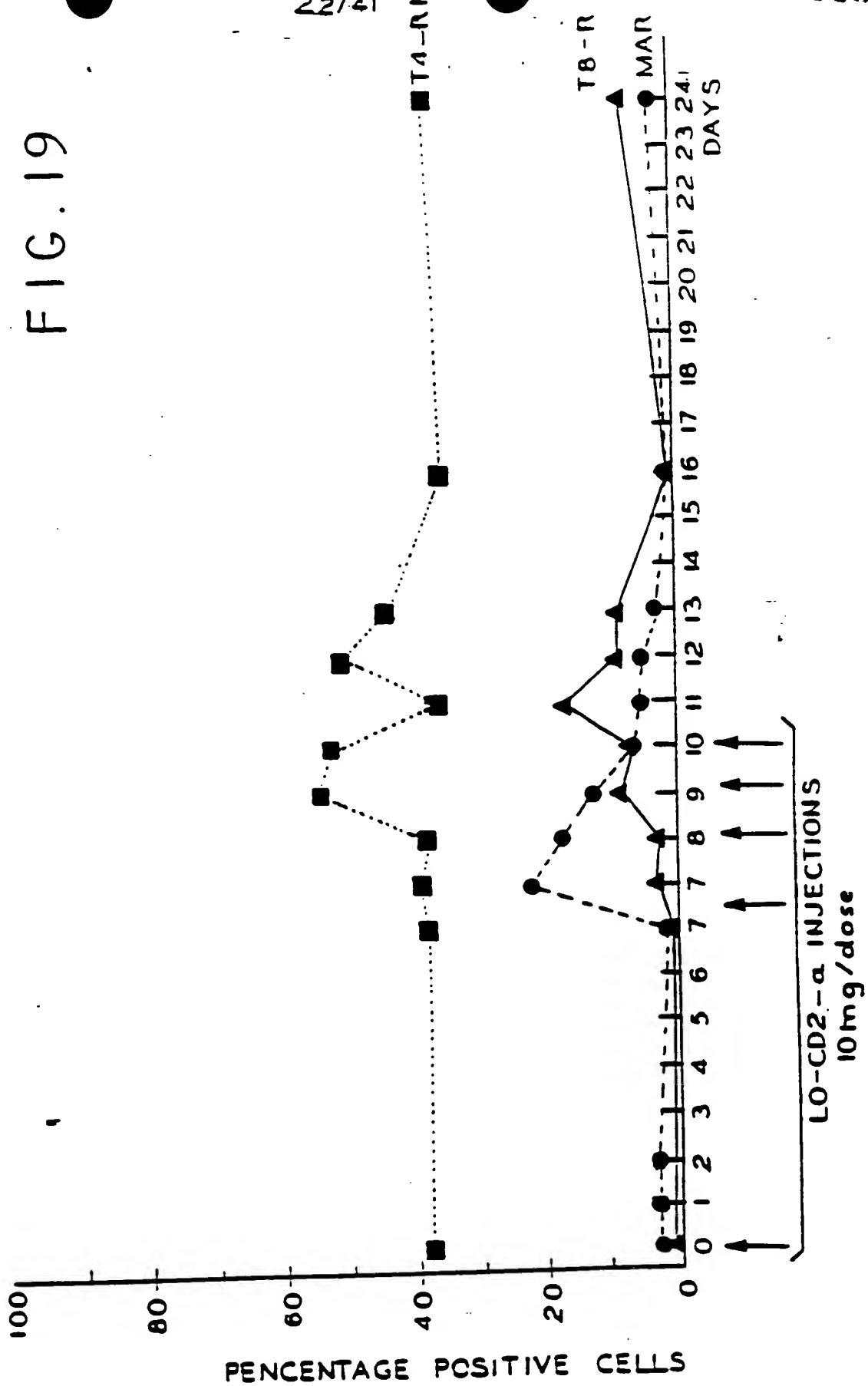
FIG. 18B



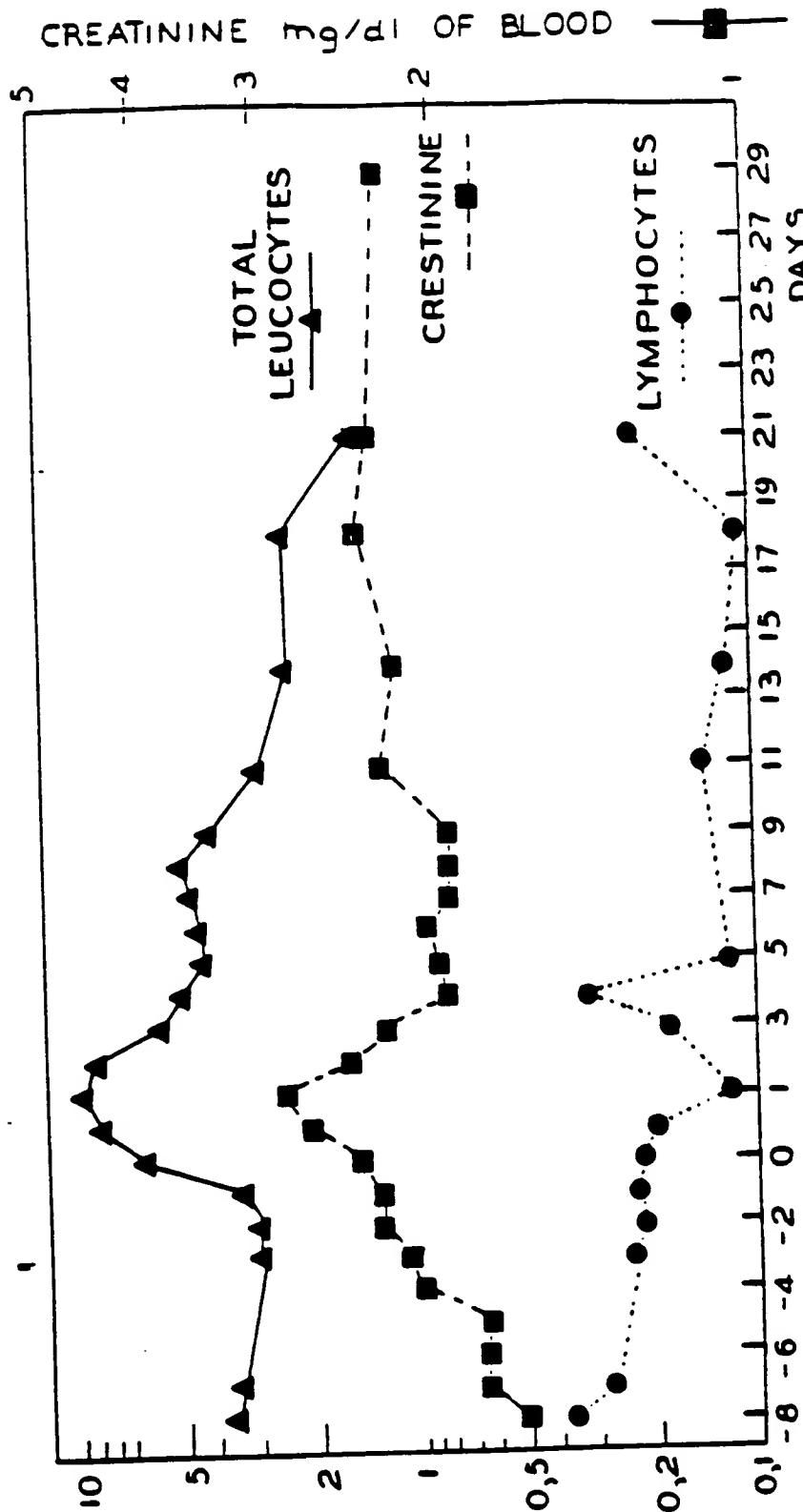
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FIG. 19



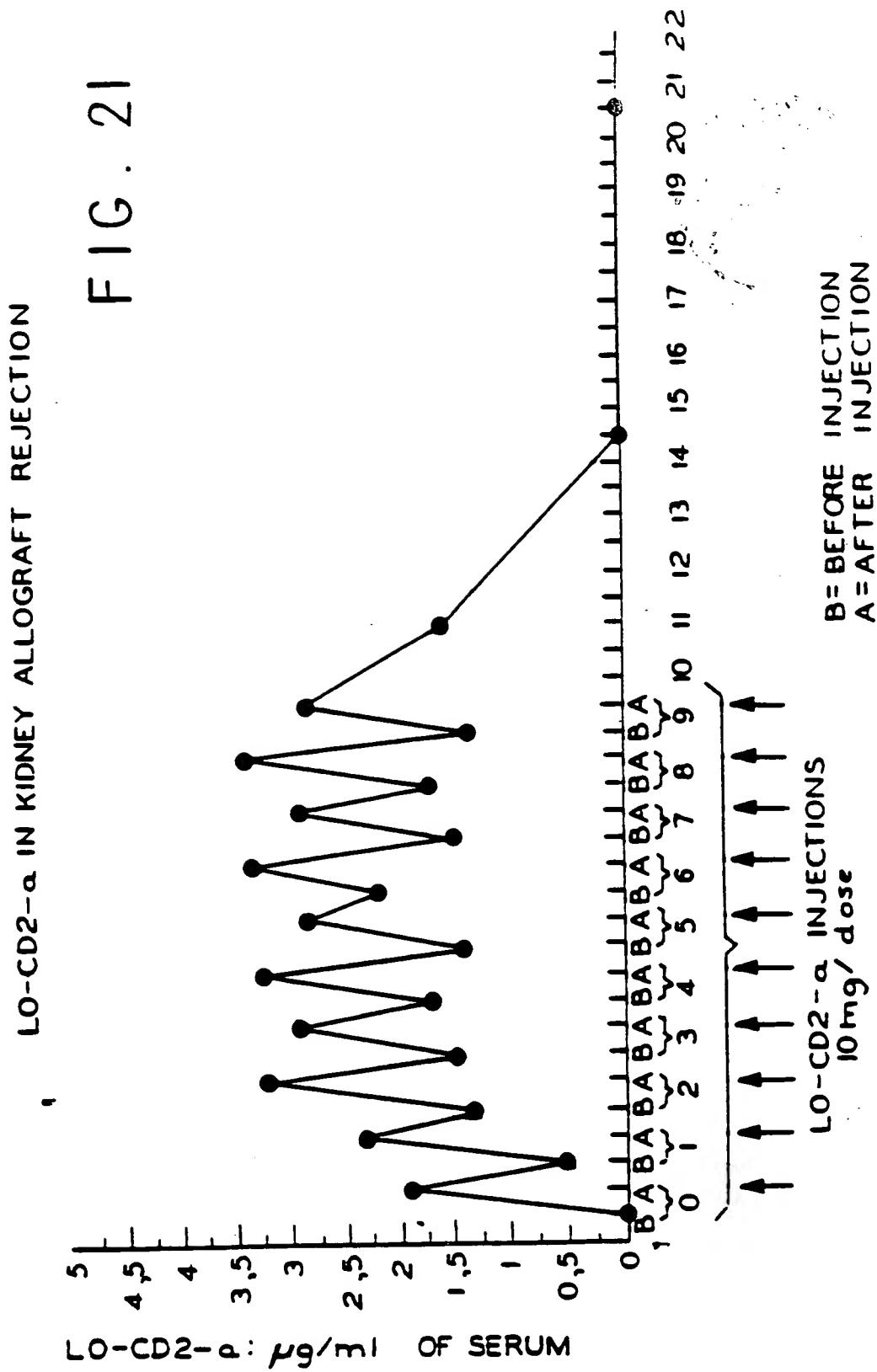
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TOTAL LEUCOCYTES → (x 10³ / ml OF BLOOD
AND TYMPHOCYTES ●

FIG. 20

FIG. 21



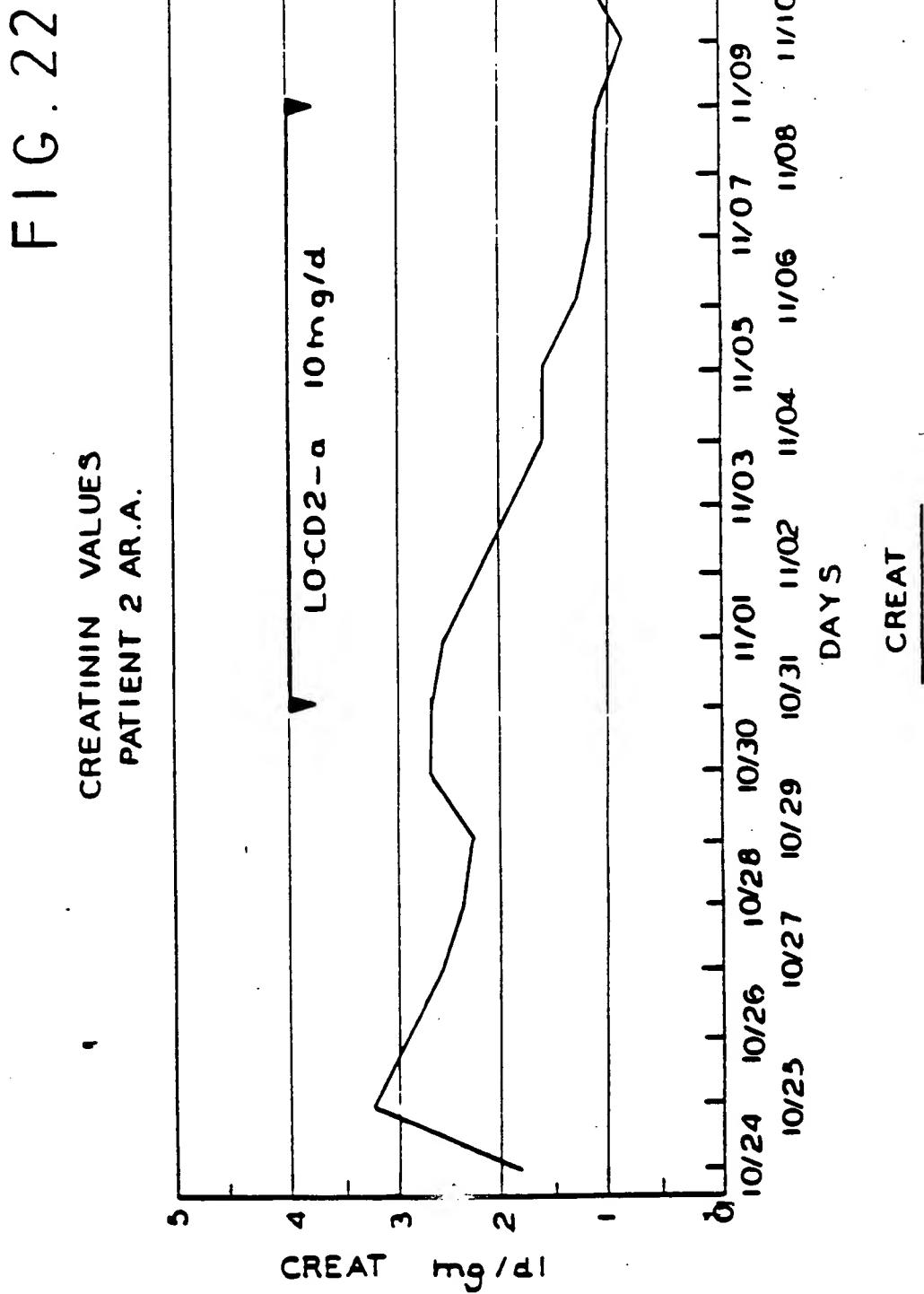
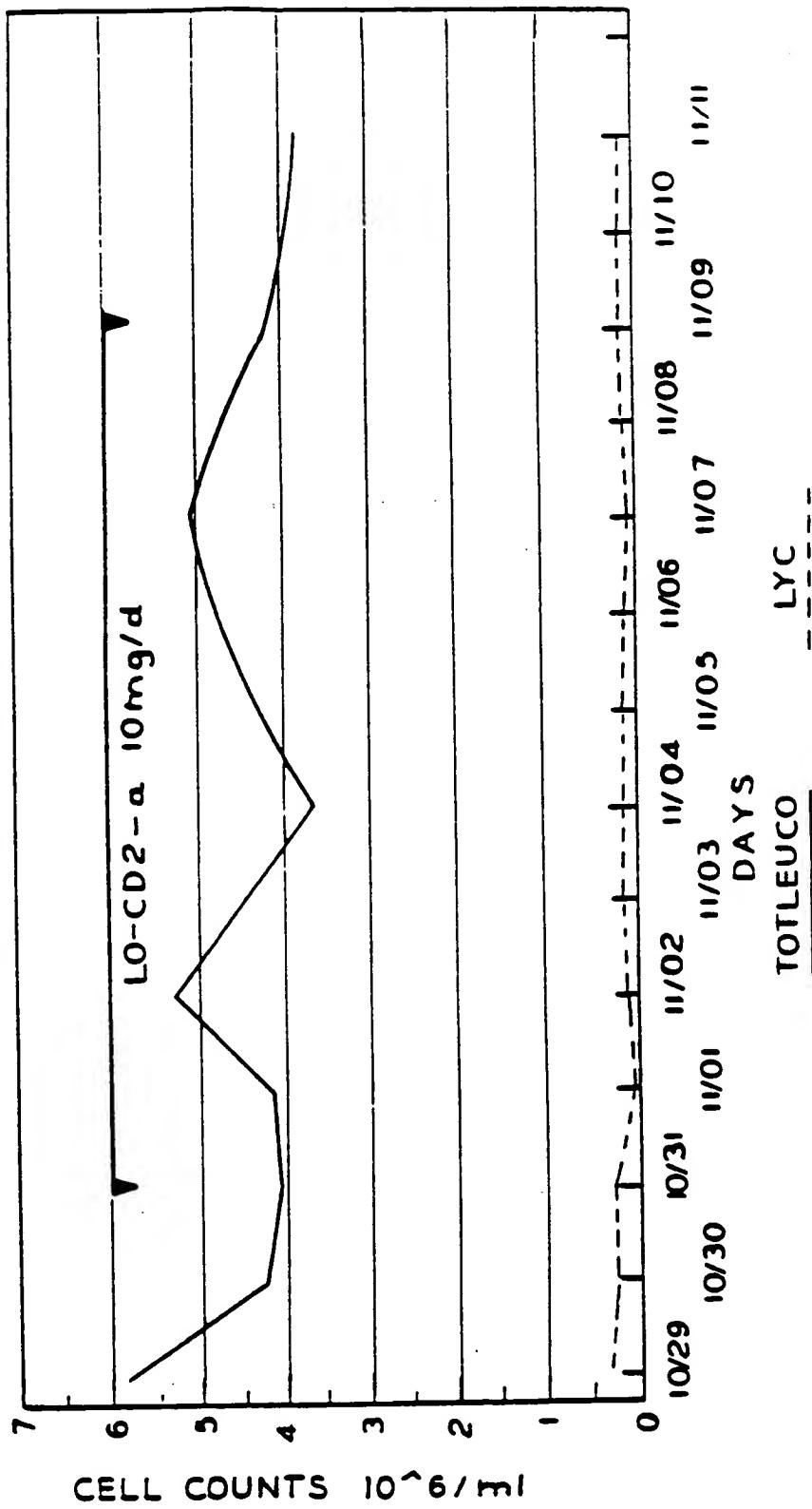


FIG. 23

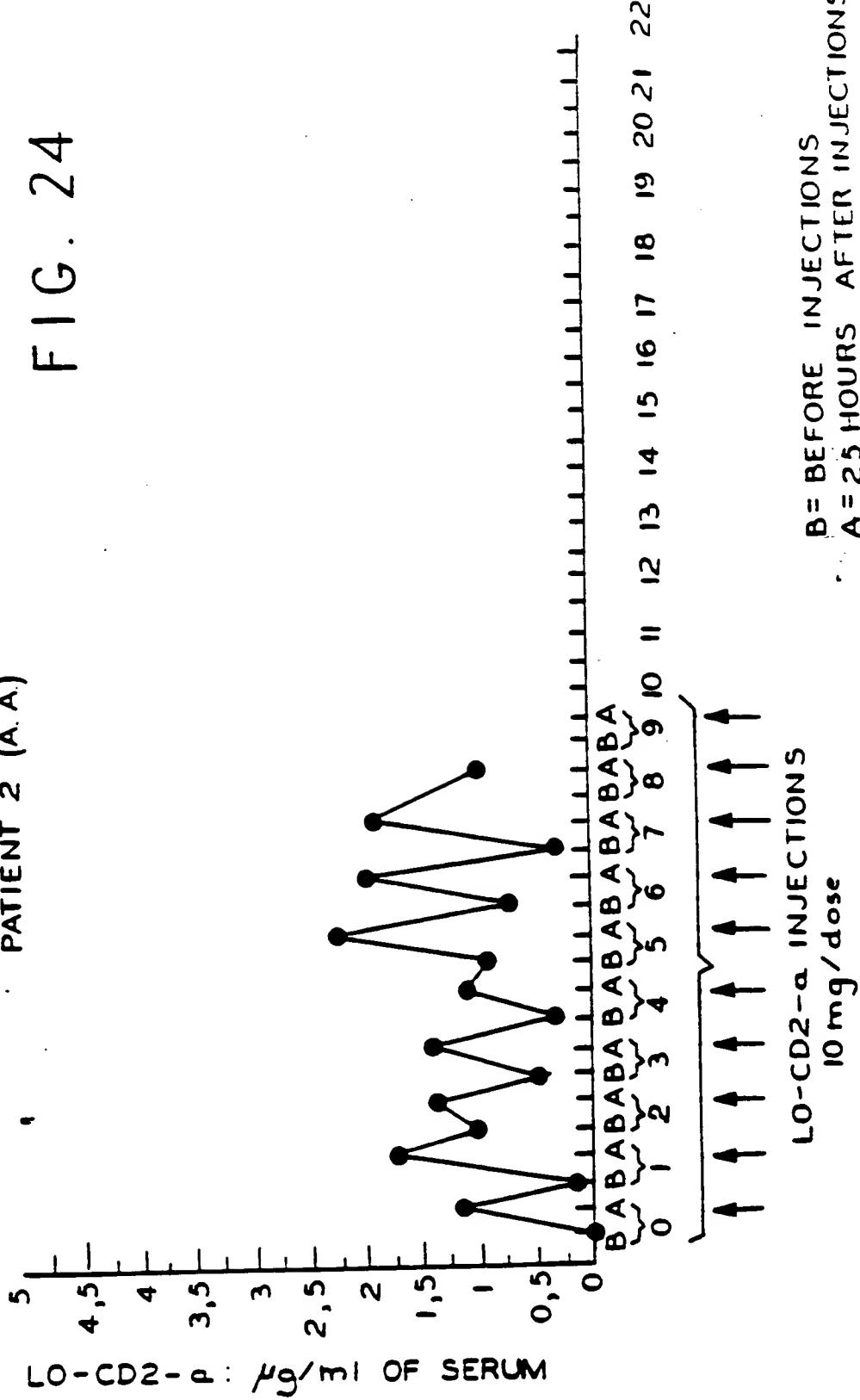
LEUCOCYTE COUNTS
PATIENT 2 A.R.A.

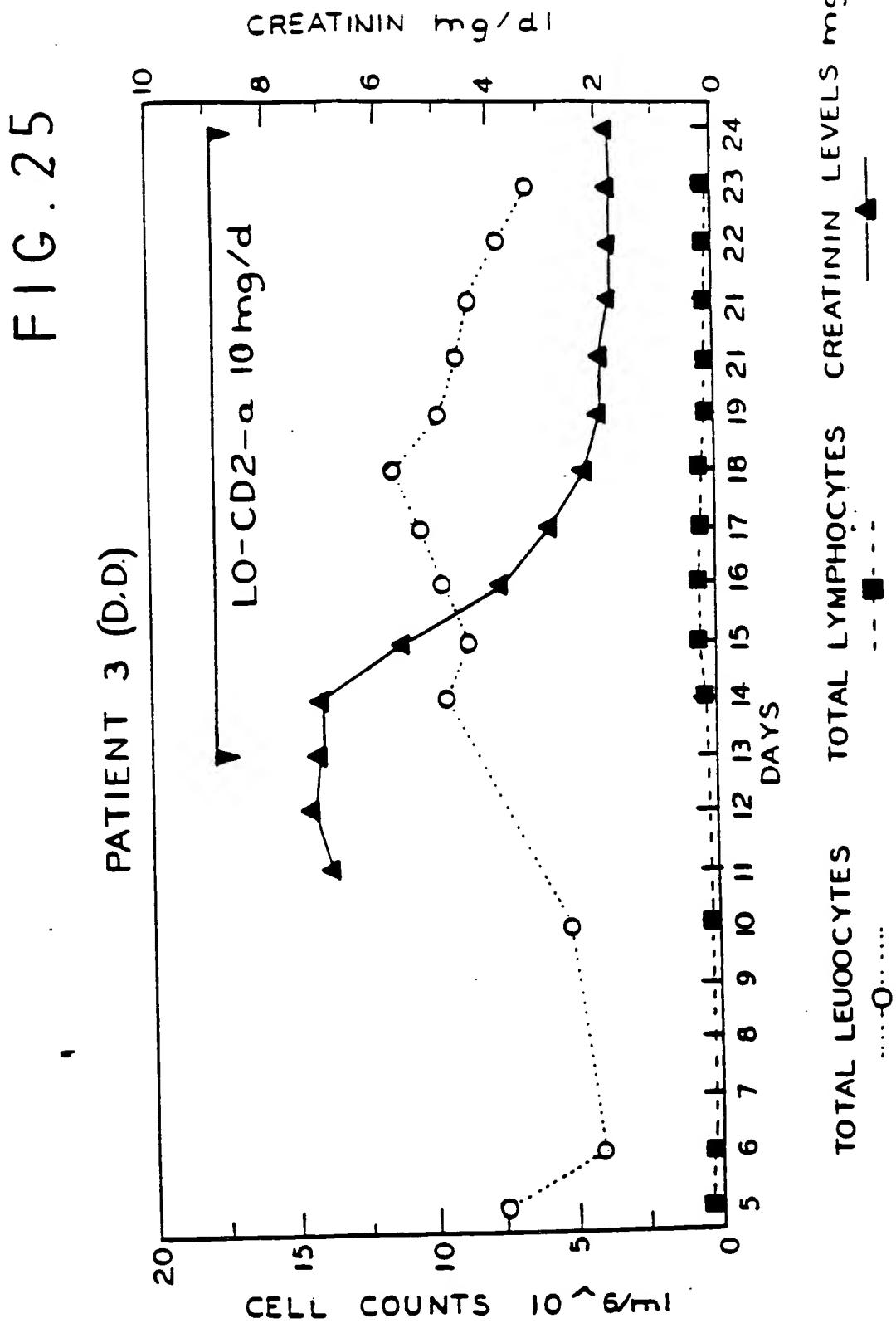


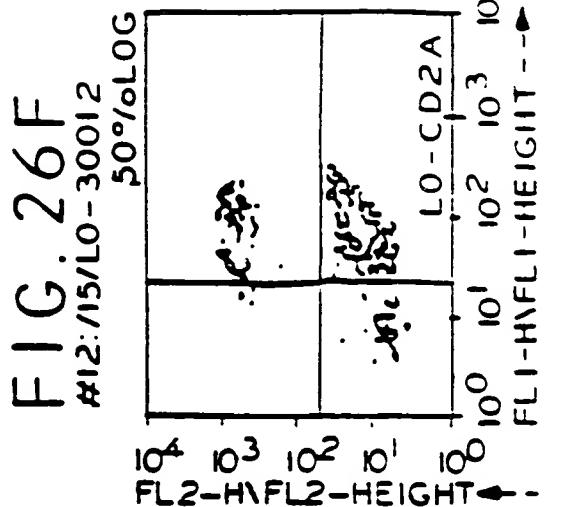
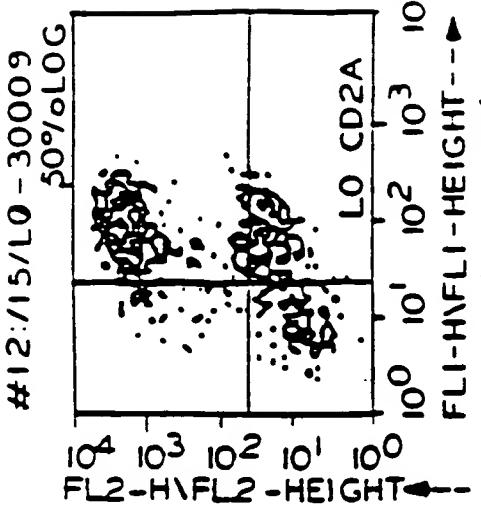
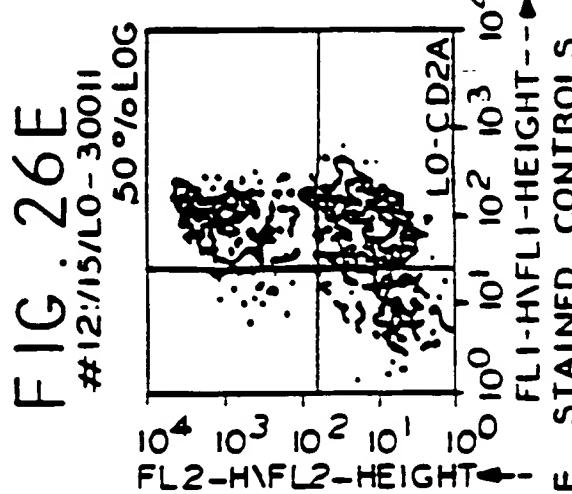
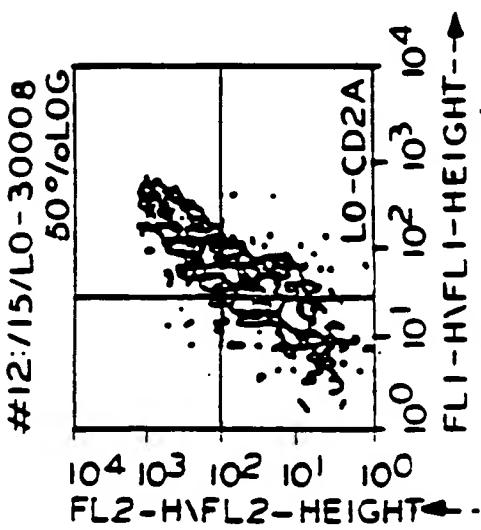
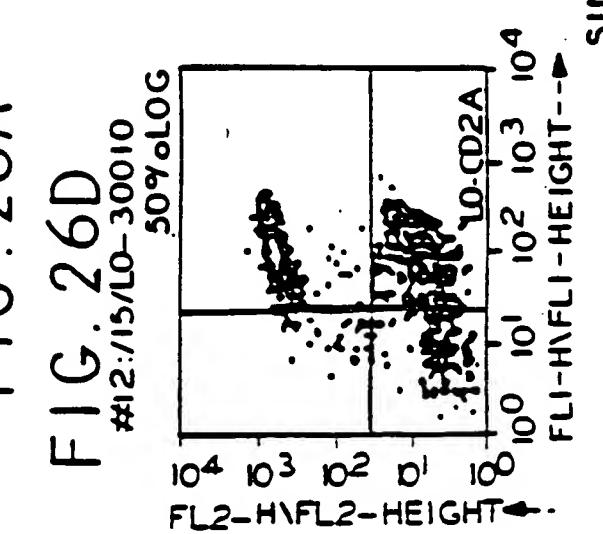
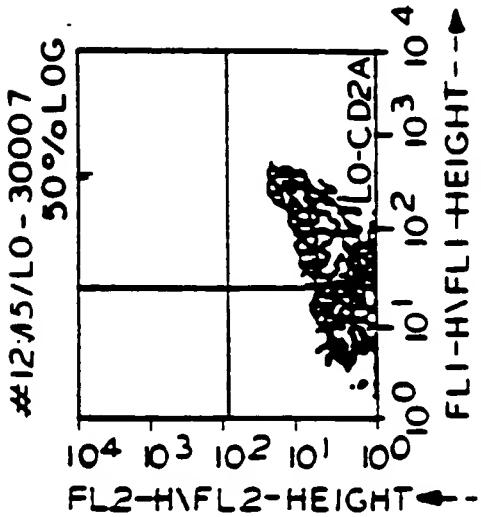
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FIG. 24

LO-CD2- α IN KIDNEY ALLOGRAFT REJECTION
PATIENT 2 (A.A.)





SINGLE STAINED CONTROLS

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SINGLE STAINED CONTROLS

#12:15/L0-300011
50%LOG

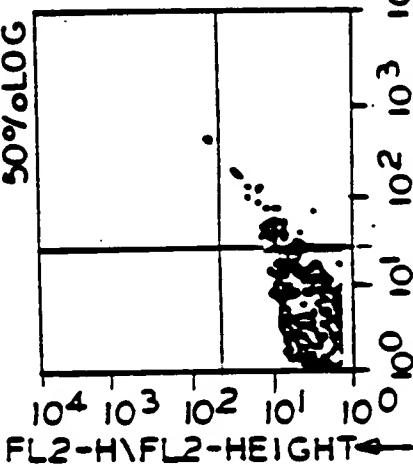


FIG. 26J

#12:15/L0-300015
50%LOG

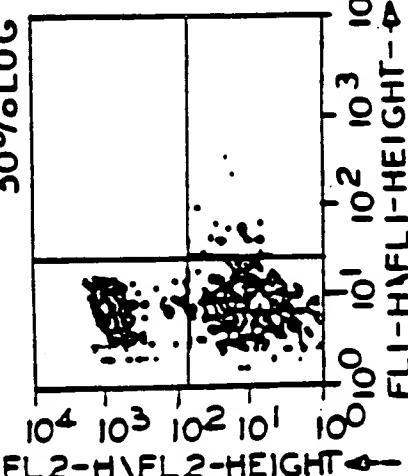


FIG. 26G

#12:15/L0-300016
50%LOG



FIG. 26H

#12:15/L0-300017
50%LOG



#12:15/L0-300013
50%LOG



#12:15/L0-300014
50%LOG

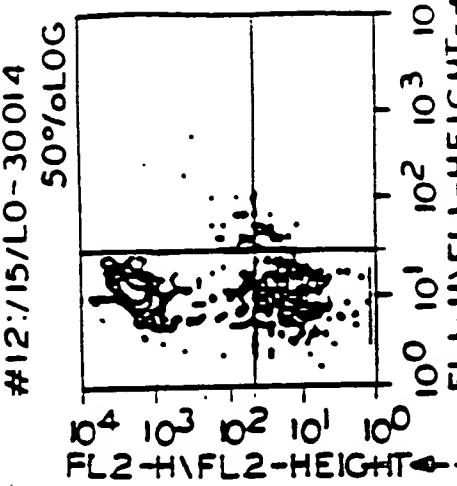


FIG. 26I

#12:15/L0-300017
50%LOG

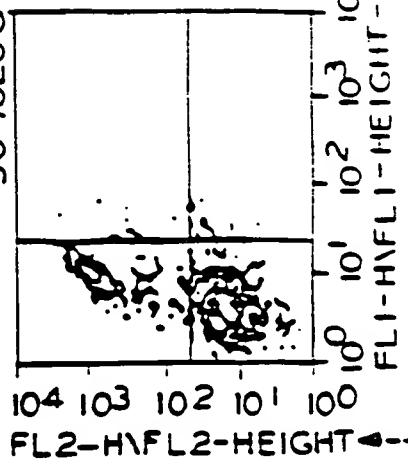
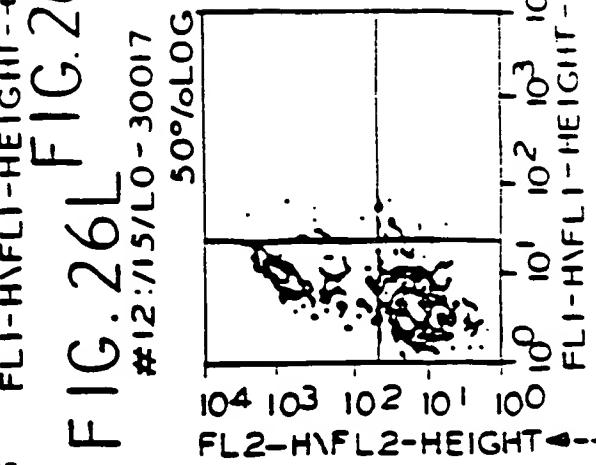


FIG. 26L

#12:15/L0-300017
50%LOG



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FIG. 27A

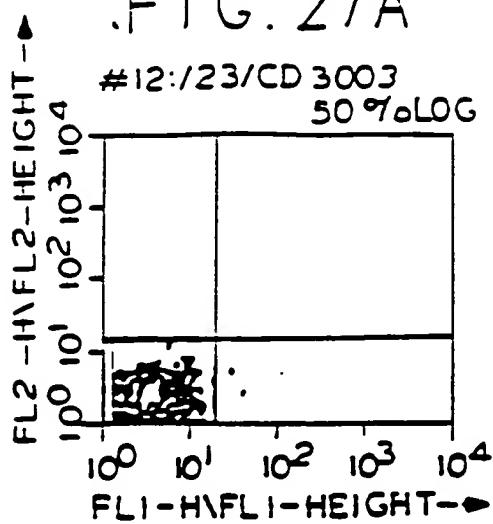


FIG. 27B

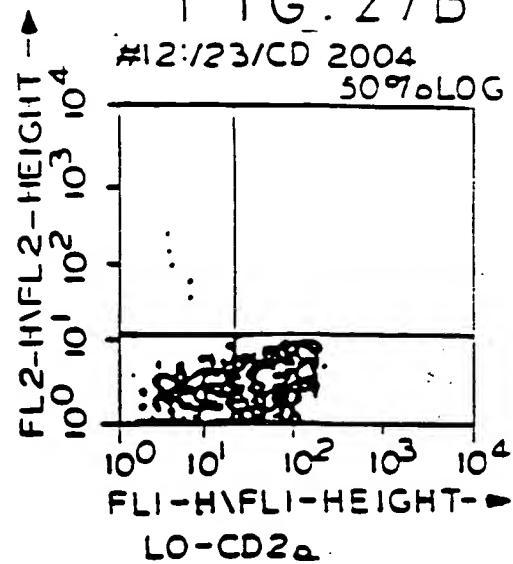


FIG. 27C

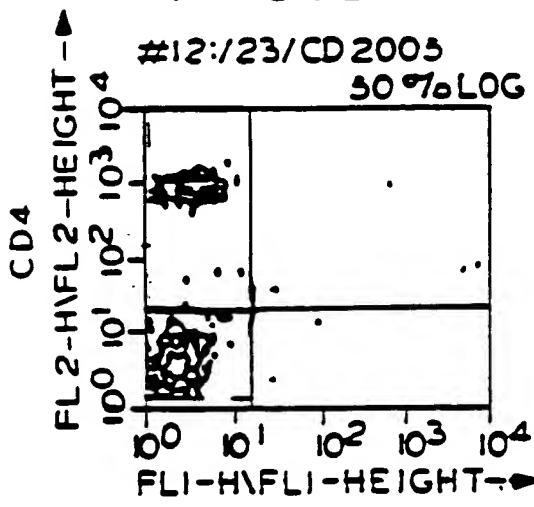


FIG. 27D

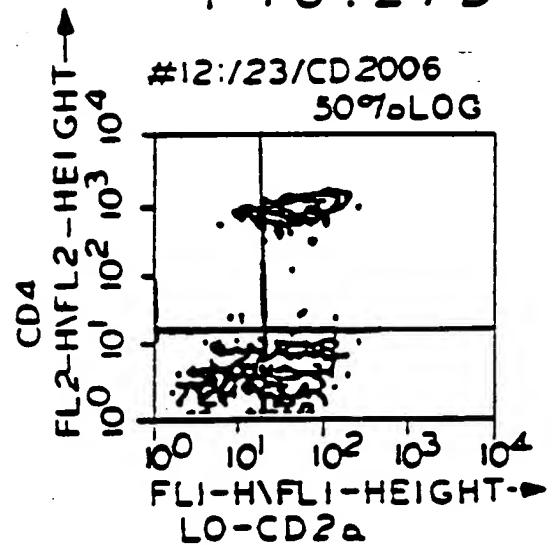


FIG. 27E

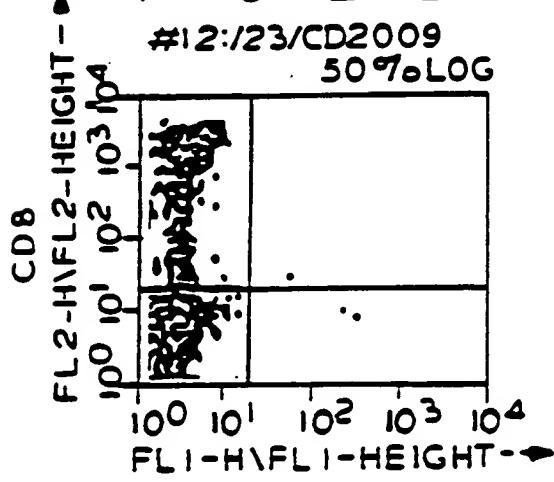
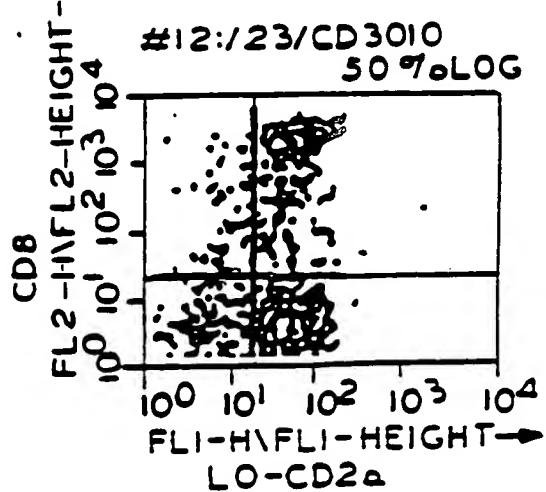


FIG. 27F



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FIG. 27G 32/41

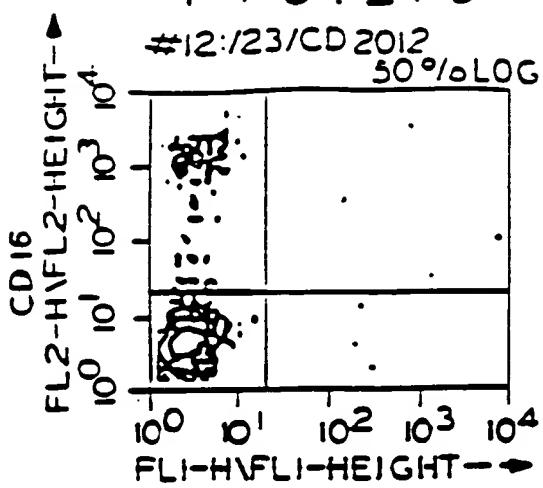


FIG. 27H

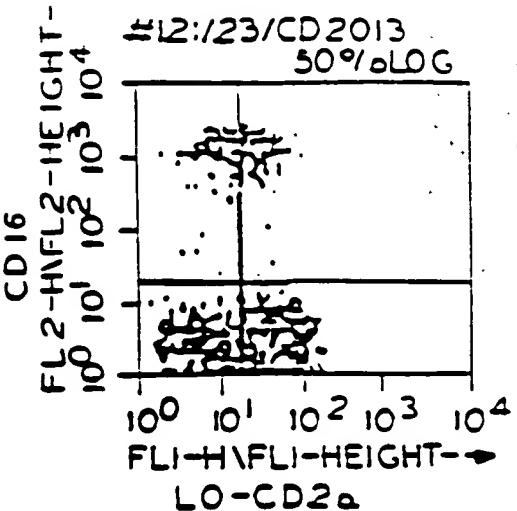


FIG. 27I

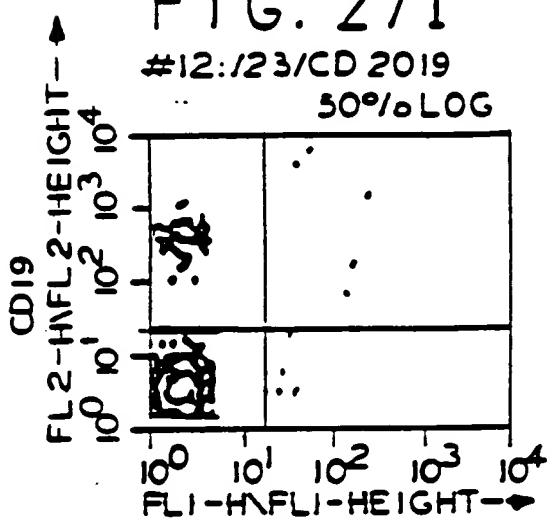


FIG. 27J

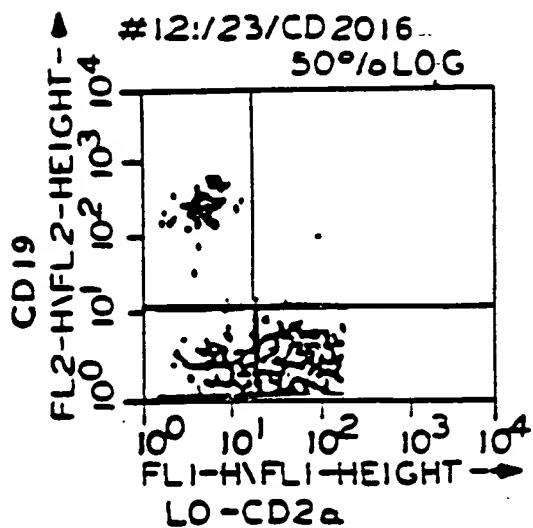


FIG. 27K

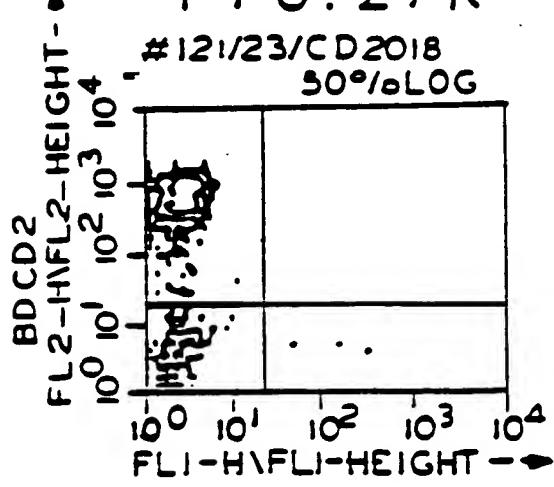


FIG. 27L

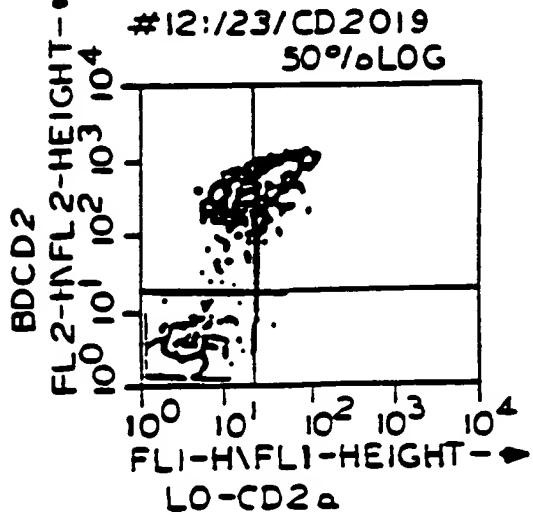
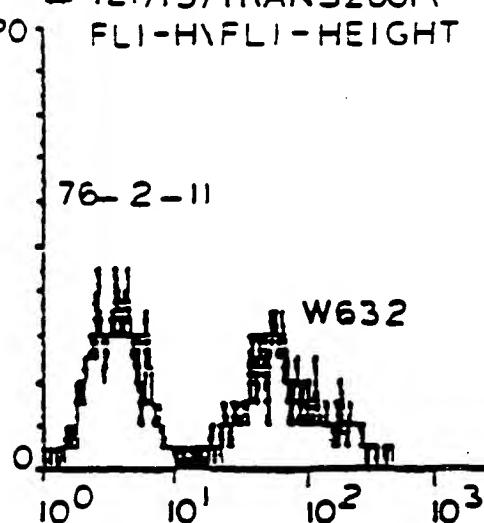


FIG. 28A

12/13/TRANS 2001\\
FLI-H\FLI-HEIGHT

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FIG. 28B

12/13/TRANS 2013\\
FLI-H\FLI-HEIGHT

76-2-11 (2%)

W632 (97%)

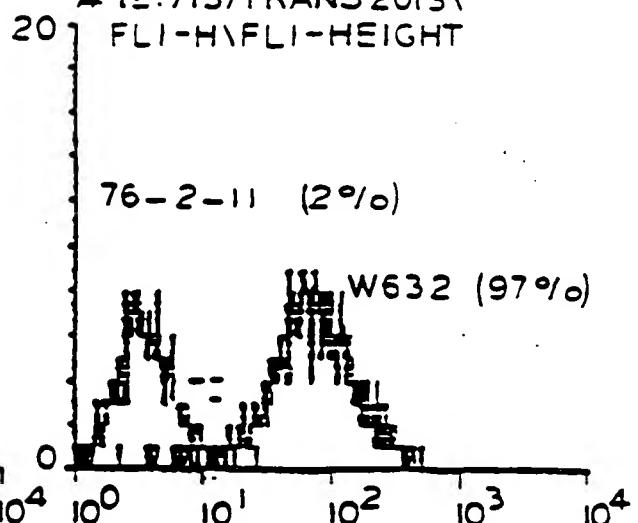


FIG. 28C

12/13/TRANS 2001\\
FLI-H\FLI-HEIGHT

76-2-11

LEU 5b

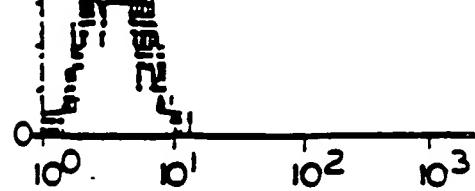


FIG. 28D

12/13/TRANS 2013\\
FLI-H\FLI-HEIGHT

76-2-11 (4%)

LEU 5b (42%)

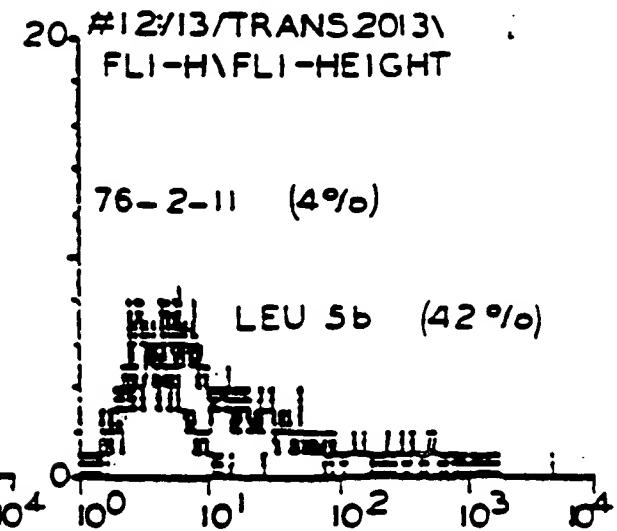


FIG. 28F

12/13/TRANS 2005\\
FLI-H\FLI-HEIGHT

RAT IgG2b

LO-CD2a

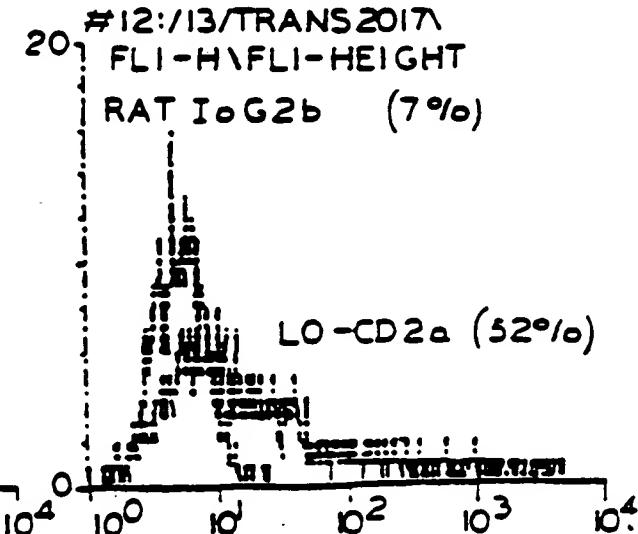


FIG. 28F

12/13/TRANS 2017\\
FLI-H\FLI-HEIGHT

RAT IgG2b (7%)

LO-CD2a (52%)



Lo-CD2a VL + Native Leader Sequence

Page 1

Sequence Range: 1 to 761

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	10	20	30	40	50	60	70	80	90	100																			
*	*	*	*	*	*	*	*	*	*	*																			
ATGATGAGTCCTGCCAGTCCCTGTTCTGTTATTGCTTGGATTCTGGTAAGTAGAGTTACAGGACAAGAATGGGATGGAGGATGAGTCT																													
M M S P V Q S L F L L L W I L G>																													
-20																													
*	110	120	130	140	150	160	170	180	190	200																			
*	*	*	*	*	*	*	*	*	*	*																			
GACTGCCCATGTTGGCTGTCATGTGGTAAGGCAGGTCTTATTCTTAAGATGGACACTTGAGATTCCATTACCTGATAATGAGAATTACAGATGAG																													
*	210	220	230	240	250	260	270	280	290	300																			
*	*	*	*	*	*	*	*	*	*	*																			
ATAGGATTGCTAAGAGGATCTAATGTTAGATGAGAAGGTGATGCCATTAGATCTGCAACCGAATTGTTGTGAAAGAACATTGCTATAACTTGTGATC																													
*	310	320	330	340	350	360	370	380	390	400																			
*	*	*	*	*	*	*	*	*	*	*																			
TTAAAATCACAAACACACGGGATCTCACAGGAATGAGTACAAAGATACTCACAGGTTGCAAATTGCTACATAACTTGTGATC																													
*	410	420	430	440	450	460	470	480	490	500																			
*	*	*	*	*	*	*	*	*	*	*																			
TATTATAATTTCAGGAACCAATGGTGTGCTGACCCAGACTCCACCTTACCTTATGGCTACCATTTGACATCAGTCTCATCTTGCAGCTCA																													
T	N	G	D	V	V	L	T	Q	T	P	P	T	L	L	A	T	I	G	Q	S	V	S	I	S	C	R	S>		
<i>10</i>																													
*	510	520	530	540	550	560	570	580	590	600	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
AGTCAGAGTCTCTTACATAGTAGTGGAACACCTATTAAATTGGTGTACAGAGGACAGGCCAATCTCCACAGGGCTATTATTGGTATCCAAAC																													
S Q S L L H S S G N T Y L N W L L Q R T G Q S P Q P L I Y L V S K>																													
*	610	620	630	640	650	660	670	680	690	700	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
TGGAAATCTGGGCCCCAACAGGTTCCAGTGGCAGTGGTCAGGAACAGATTCAACTCAAATCAGTGGAGTGGAAAGCTGGATTGGGGTTATTAA																													
L E S G V P N R F S G S G T D F T L K I S G V E A E D L G V Y Y>																													
<i>10</i>																													
*	710	720	730	740	750	760	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
CTGCATGCCATTACCCATATCCGTACACGTTGGAGCTGGACCAAGCTGGACTGAA																													
C M Q F T H Y P Y T F G A G T K L E L K>																													
<i>100</i>																													

Fig-29

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Sequence Range: 1 to 491

ATGAAATCCAGGATCATCCTCTTCTGATGCCAGTACAGGCACTCCAACTGAGAGATCATACCTGGAGACAGTA
 M K C R W I I L F L M A V A T G>
 -19

* * * * * 20 * * * * * 30 * * * * * 40 * * * * * 50 * * * * * 60 * * * * * 70 * * * * * 80 * * * * * 90 * * * * * 100
 CACTATCTTGGATTCTTCAACAGGGTCAACTCAGAAGTCAGGCTCAGCAATCTGGGCCTGAGCTTCAGAGACCCCCGGGCTCAGTCAGTGTGCG
 V N S E V Q L Q Q S G P E L Q R P G A S V K L S>
 1
 * * * * * 220 * * * * * 230 * * * * * 240 * * * * * 250 * * * * * 260 * * * * * 270 * * * * * 280 * * * * * 290 * * * * * 300
 TGCAGGGCTCTGGCTATATATTACAGAACTATATGTAATGGGTGAAGCAGAGGCCTAACAGGGCCTGGATTAGGAAGGATCGATCCCTGAAG
 C K A S G Y I F T E Y Y M Y W V K Q R P K Q G L E L V G R I D P E>
 30
 * * * * * 310 * * * * * 320 * * * * * 330 * * * * * 340 * * * * * 350 * * * * * 360 * * * * * 370 * * * * * 380 * * * * * 390 * * * * * 400
 ACGGTAGTATTGATTATGTTGAGAACTTCAAAAGAAGGCCACACTGCACTACATCGTCCACACACCCCTACATGCAACTCAGGACCTGACATC
 D G S I D Y V E K F K K K A T L T A D T S S N T A Y M Q L S S L T S>
 60
 * * * * * 410 * * * * * 420 * * * * * 430 * * * * * 440 * * * * * 450 * * * * * 460 * * * * * 470 * * * * * 480 * * * * * 490
 TGAGGACACAGCACCTATTGCTAGGGAAATCAACTATCGATTGCTTACTGGGCCAACGCCACCCCTCGTCACAGTCTCCCTA
 E D T A T Y F C A R G F N Y R F A Y W G Q G T L V T V S S>
 180

Figure 30

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Light Chain Variable Region Sequences of rat LO-CD2a,
human HUM5400, and humanized LO-CD2a

	FR 1	CDR 1	FR 2
	* * 20	30	40 **
Rat LO-CD2a Vk	DVVLTQTPPT LLATIGQSVS ISCRSSQSLL HSSGNTYLNW LLQRTCQSPQ		
Humanized Vk	---M---S---S ---V-L---PA-	-----	-----P-----
Human HUM5400 Vk	---M---S-LS -PV-L---PA-	-----V Y-D---H--- FQ---P---R	
	CDR 2	FR 3	CDR 3
	* 60	70 80	90 100
Rat LO-CD2a Vk	PLIYLVSKLE SGVPNRFSGS GSGTDFTLKI SGVEAEDLGV YYCMQFTHYP		
Humanized Vk	-----D-----	-----V-----	
Human HUM5400 Vk	R---K---NRD ---D-----	-----R---V-----G---W	
	FR 4		31
	110		
Rat LO-CD2a Vk	YTFGAGTKLE LK		
Humanized Vk	---Q----- I-		
Human HUM5400 Vk	---Q----- I-		

Humanized LO-CD2a Light Chain V Region

Sequence Range: 1 to 807

10	20	30	40	50	60	70	80	90	100
*	*	*	*	*	*	*	*	*	*
AAGCTTCATGATGAGTCCTGTCAGTCCTGTTCTGGATTATGCTTAAGTAGAGAATGAGTTACAGGACAAGAATGGGATGGGAGAT									
M	M	S	P	V	Q	S	L	F	L
110	120	130	140	150	160	170	180	190	200
*	*	*	*	*	*	*	*	*	*
GAGTTCTGACTGCCCCATGGTGGCTGTCATGTTGGTAAAGGCAGGGTCCATTAGATGGACACTTGTAGATTCTAAGATGGAGATTCTGATAATGAGAAATTAC									
210	220	230	240	250	260	270	280	290	300
*	*	*	*	*	*	*	*	*	*
AGATGAGATAGGGATTGGCTAAGAGGATTCTAAATGTAAGATGAGAAGGGTATGAGTTACAGGGAAATGAGGTAACAAAAAGTAATTTCACAAAGAGATTGGTTGCAAAATTTCACATAACTTGT									
310	320	330	340	350	360	370	380	390	400
*	*	*	*	*	*	*	*	*	*
ATATTTTTAAATCACAAAACACACCGGGATCTCACAGGGAAATGAGGTAACAAAAAGTAATTTCACAAAGAGATTGGTTGCAAAATTTCACATAACTTGT									
410	420	430	440	450	460	470	480	490	500
*	*	*	*	*	*	*	*	*	*
TCTGATCTATTATTCAGGAACCAATGGTGTGTTGTGACCCAGAGTCACCTTCATTATTGGTAACCTTGCATCTCTCTTG									
T	N	G	D	V	M	T	Q	S	P
510	520	530	540	550	560	570	580	590	600
*	*	*	*	*	*	*	*	*	*
CAGGTCAAGTCAGAGTCCTCTACATAGTAGTGGAAACACCTATTAAATTGGTTGCTACAGAGGCCAACATCTCCACAGGCCAACATTATTTCAGTCGA									
R	S	S	L	H	S	S	N	T	Y
610	620	630	640	650	660	670	680	690	700
*	*	*	*	*	*	*	*	*	*
TCCAAACTGGAAATCTGGGGTCCCCGACAGGTTCACTGGCTCAGGGAGTGGAACAGGATTTCACACTCAAATCAGTGGAGTGGAAAGCTGAGGATGGGGG									
S	K	L	E	S	G	V	P	D	F
710	720	730	740	750	760	770	780	790	800
*	*	*	*	*	*	*	*	*	*
TTTATTACTGCATGCAATTACCCATTATCCGTACACGTTGGACAAGGGACCAAGCTGGAAATCAAACGTTGAGTAGAAATTAAACTTTGCTTCCTCAGT									
V	Y	C	M	Q	F	T	H	P	I
*	*	*	*	*	*	*	*	*	*
TGGATC									

Fig. 32

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**Heavy Chain Variable Region Sequences of rat LO-CD2a,
human Amu 5-3, and humanized LO-CD2a**

	FR 1	CDR 1	FR 2
	10 20	30 40	* 50
Rat LO-CD2a Vh	EVQLQQSGPE LQRPGASVKL SCKASGYIFT EYYMYWVKQR PKQGLELVGR		
Humanized Vh	Q---V---A- VKK-----V -----T-- -----R-A -G-----M--		
Human Amu 5-3 Vh	Q---V---A- VKK-----V -----T-- G---R---R-A -G-----W---		
	CDR 2	FR 3	
	60 * * * * 80 * * 90 100		
Rat LO-CD2a Vh	IDPEDGSIDY VEKFKKKATL TADTSSNTAY MQLSSLTSED TATYFCARGK		
Humanized Vh	----- -----V-- -----S-- -E-----D- --V-Y-----		
Human Amu 5-3 Vh	-N-NS-GTN- AQ--QGRV-M -R---IS--- -E--R-R-D- --V-Y---R		
	CDR 3	FR 4	
	110		
Rat LO-CD2a Vh	FNYR//FAYWGQ GTLTVSS		
Humanized Vh	----//----		
Human Amu 5-3 Vh	TE-IVVAEG-D---		

Fig. 33

Fig. 34

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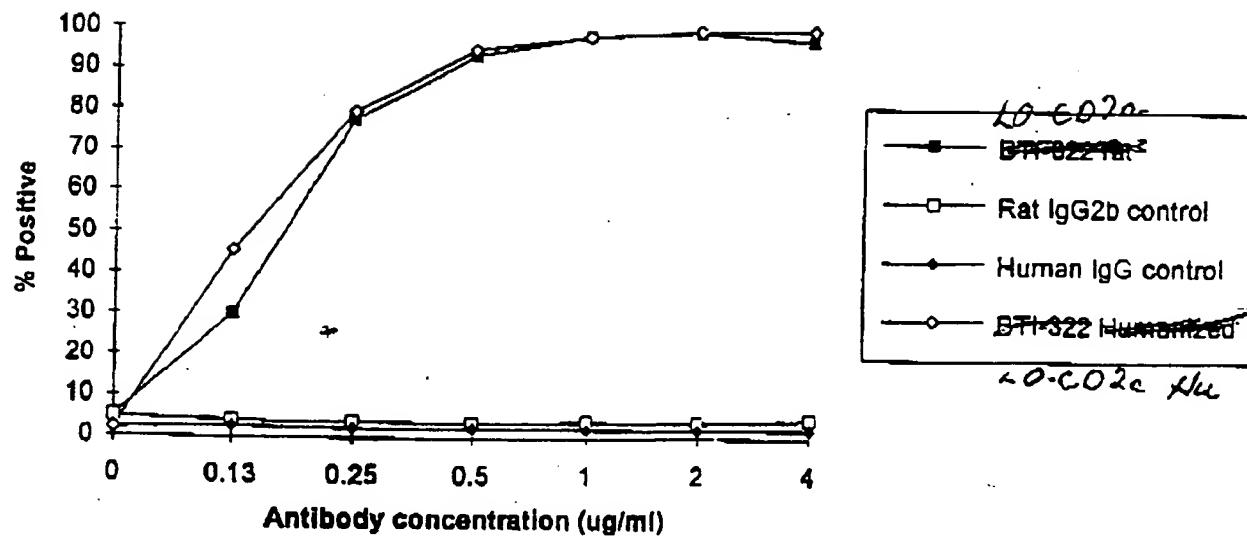
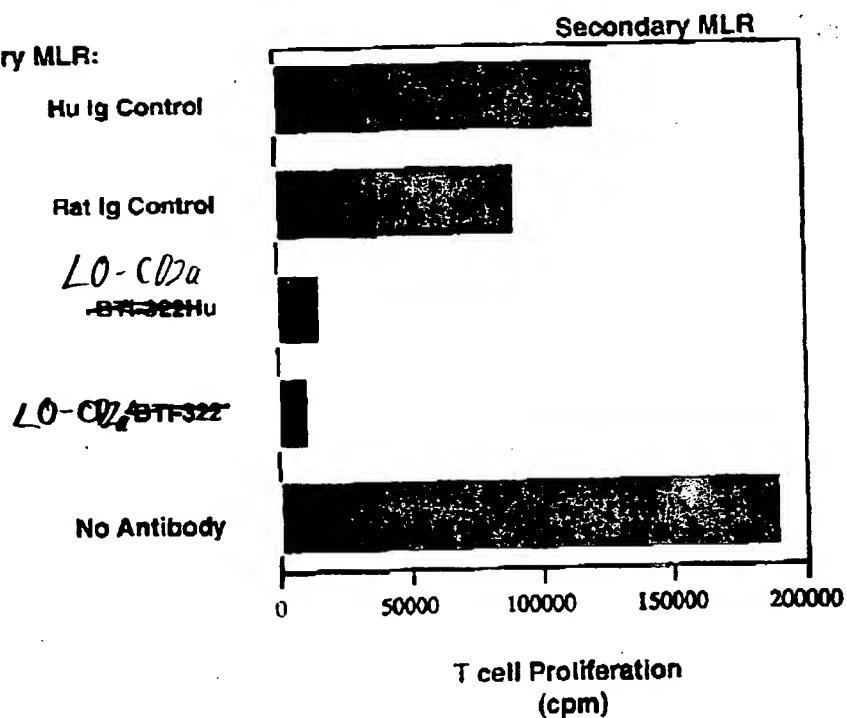
Binding of LO-CD2a and LO-CD2a Hu
to Jurkat Cells

Fig. 35

Induction of Hyporesponsiveness *in vitro*

Additions to primary MLR:

Fig.
3.6

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A.

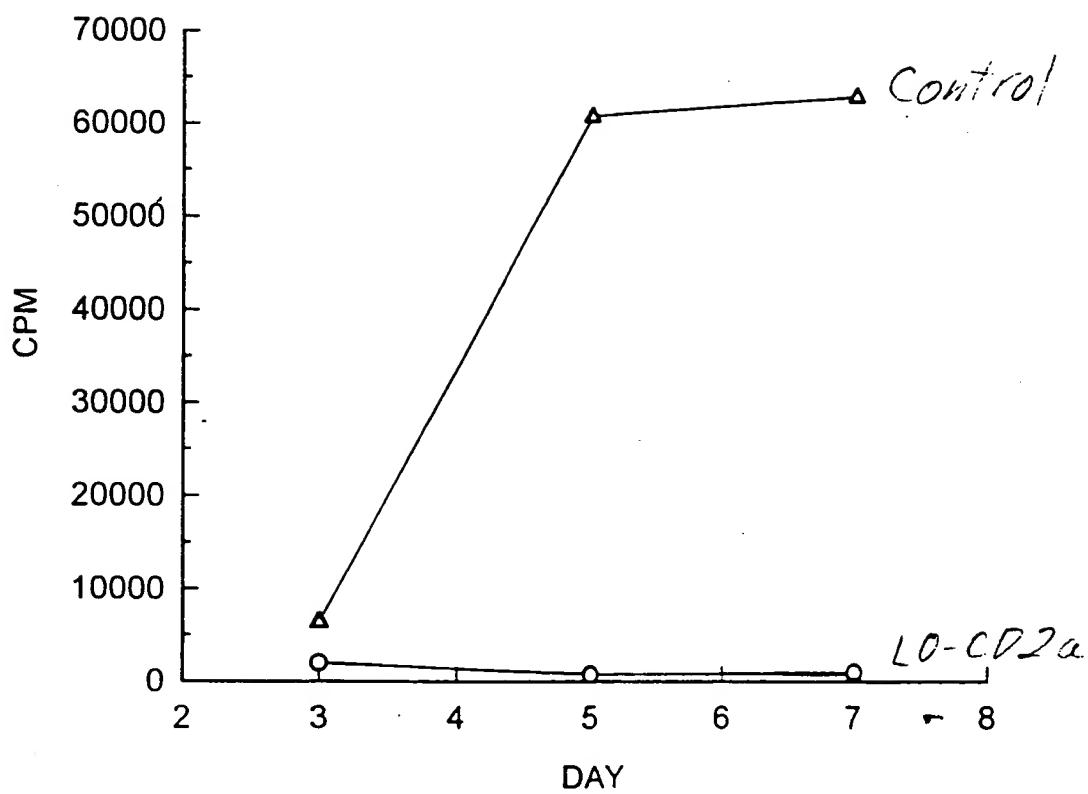
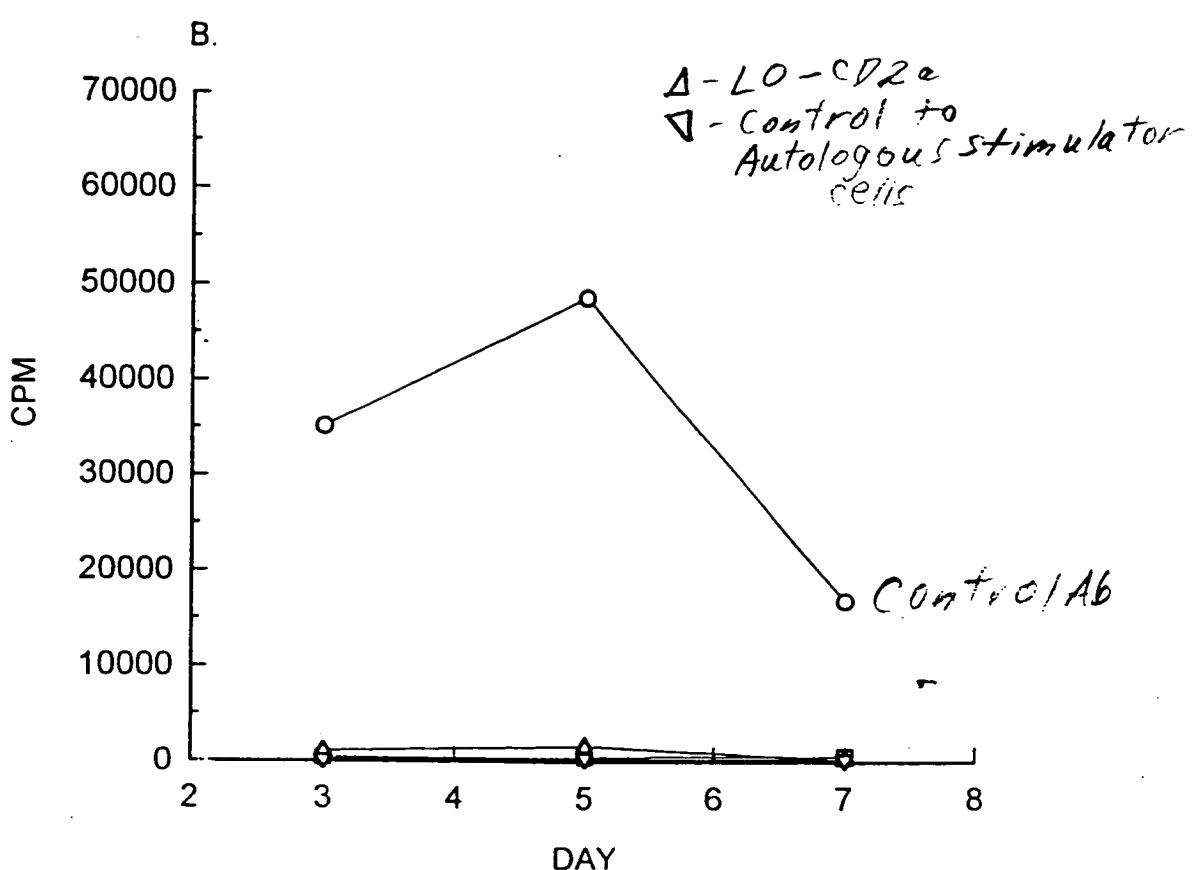


Fig. 37A



110 378

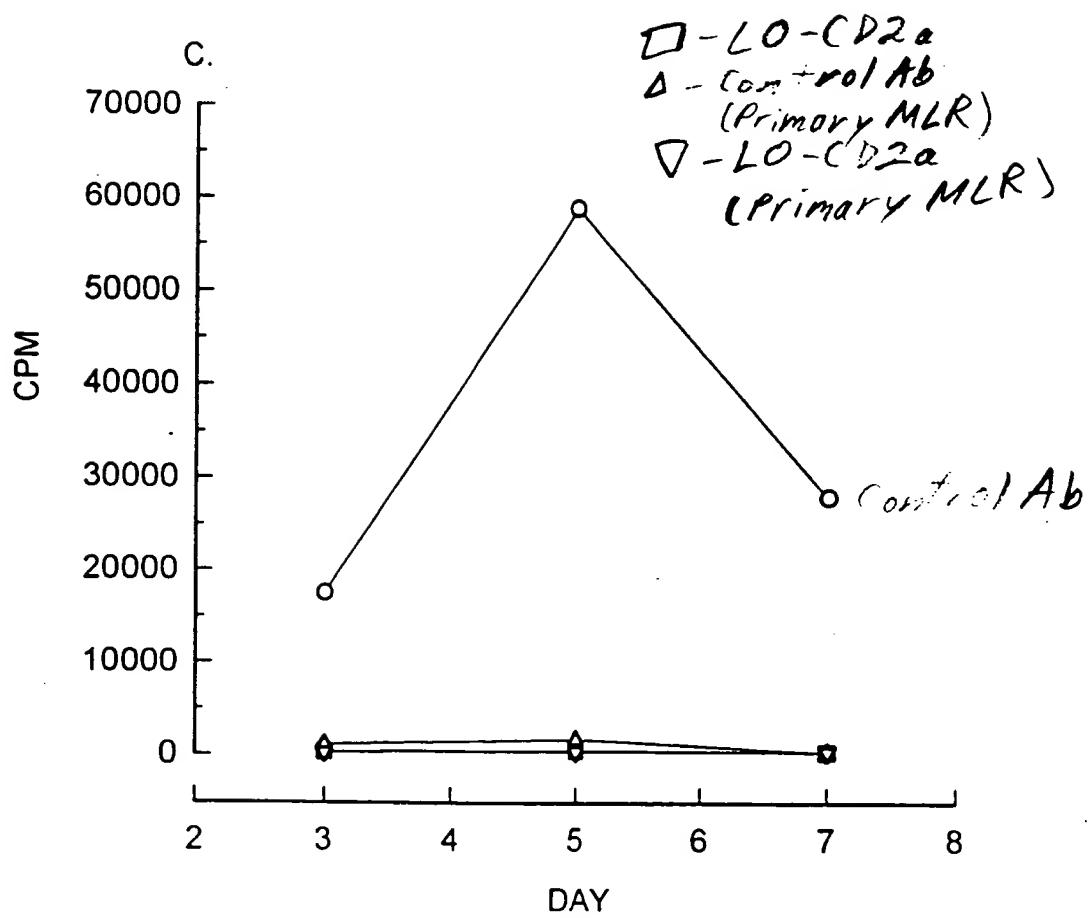


Fig. 37C

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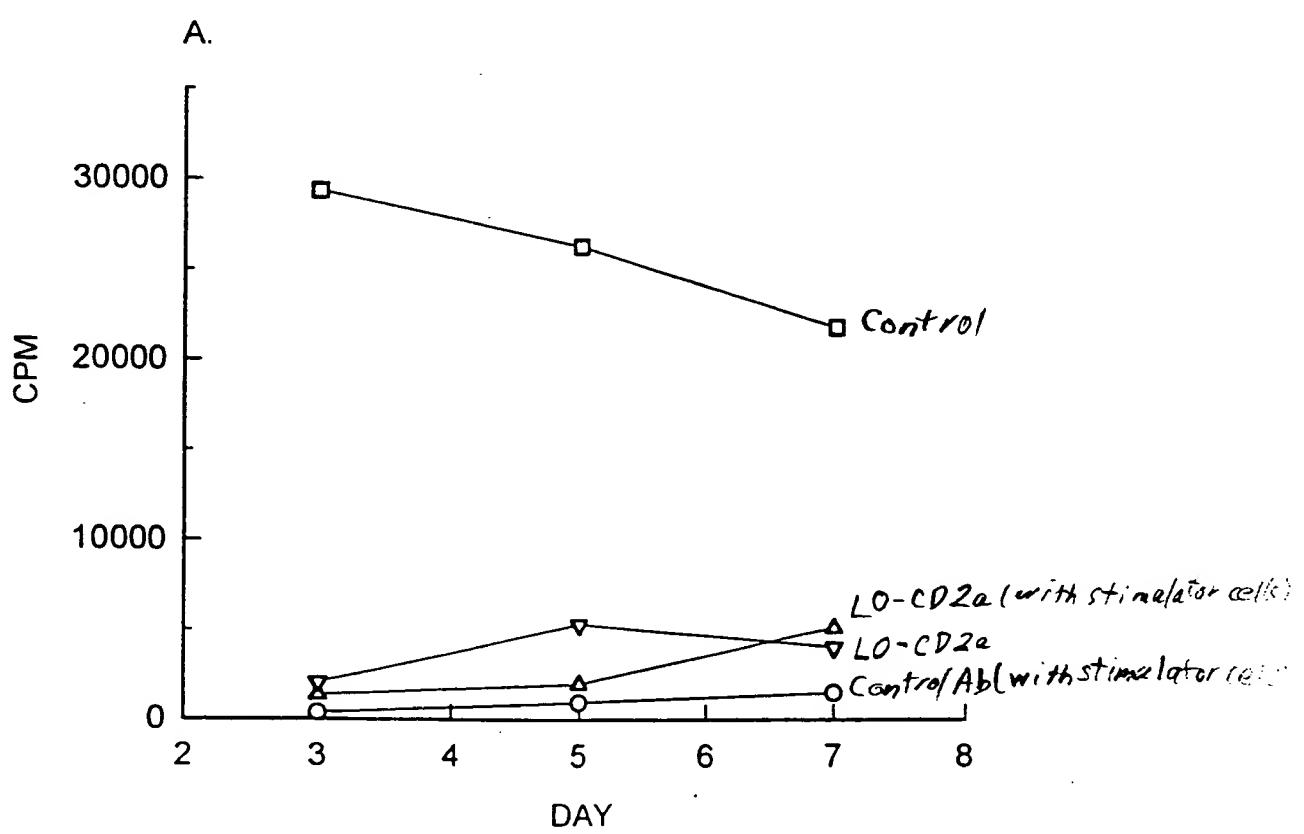


Fig. 38A

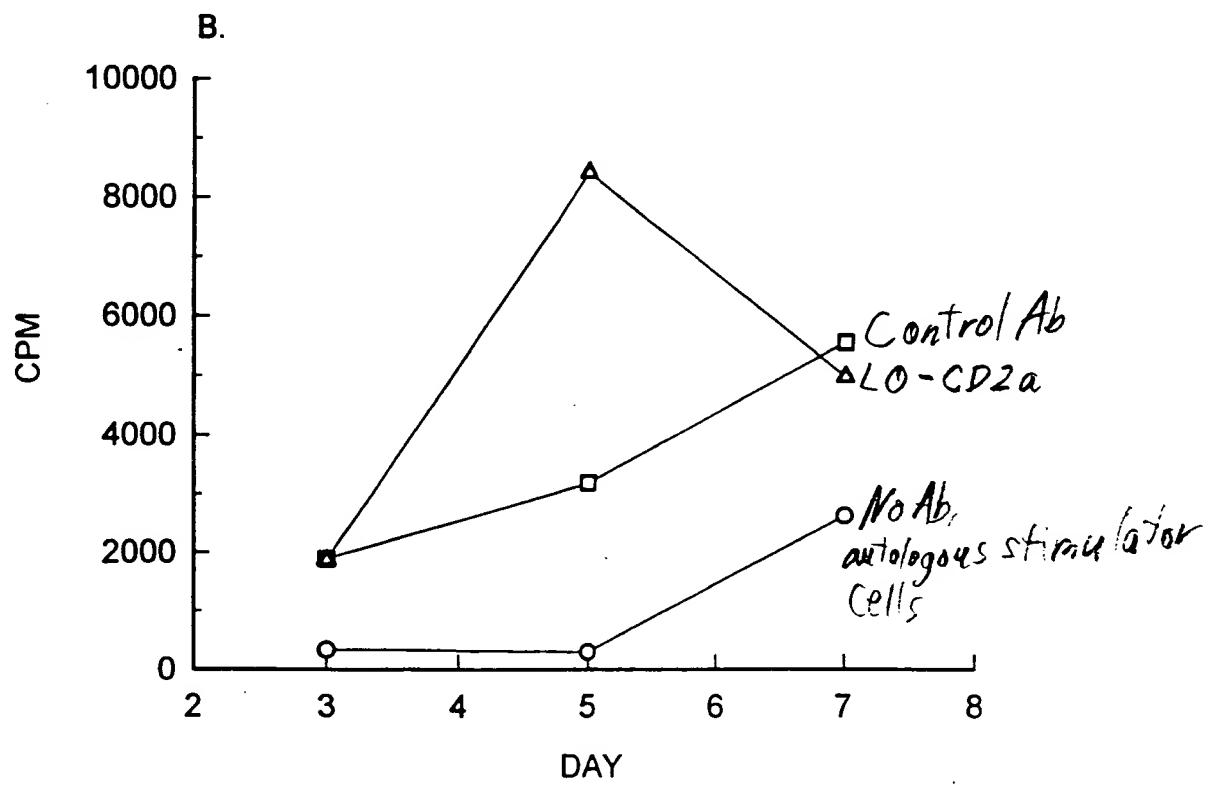


Fig. 38B

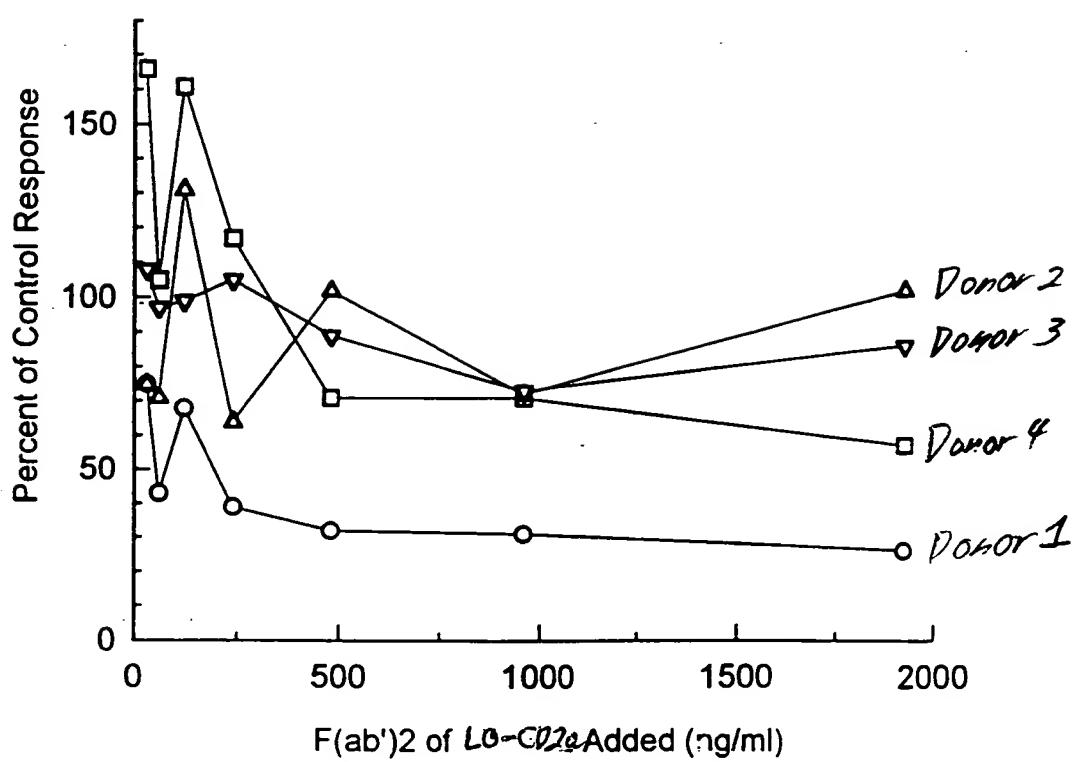


Fig. 39

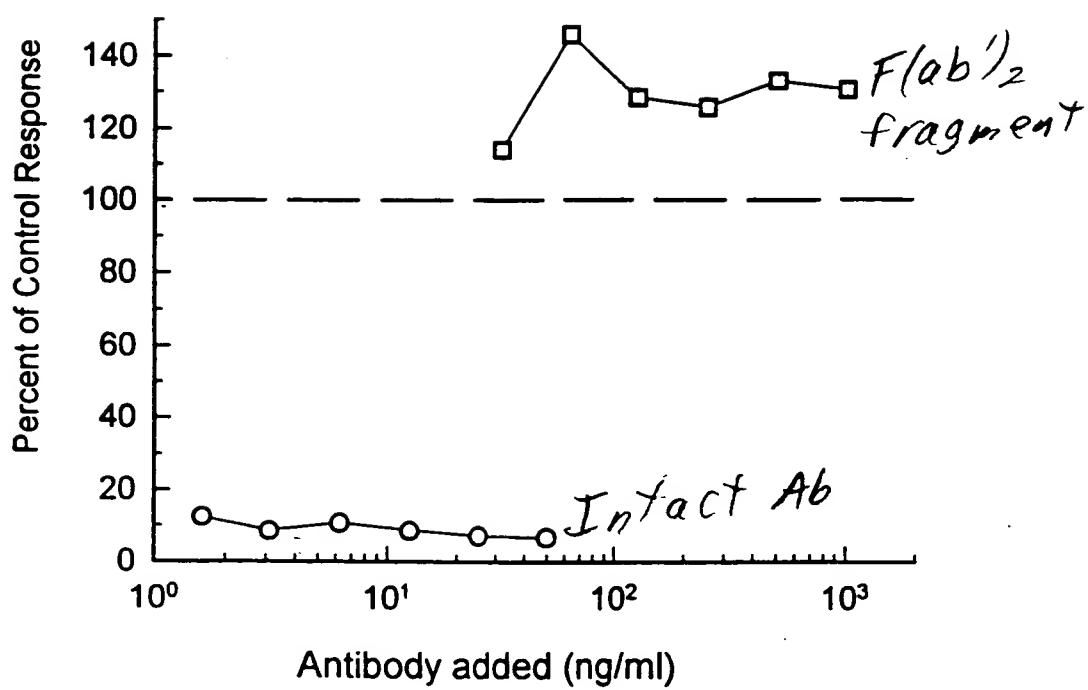


Fig. 40

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